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nucleic search, using sw model

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March 5, 2006, 17:08:23; Search time 872.437 Seconds (without alignments) 10014.946 Million cell updates/sec

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ALIGNMENTS

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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Total number of hits satisfying chosen parameters:

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4996997 seqs, 3332346308 residues

Searched:

Scoring table: Sequence: Perfect score: Title:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxing, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile

DR WPI; 1999-105628/09.		XX PR 23-JUN-1997;	XX PF 19-JUN-1998;	30-DEC-1998.	WO9859061-A1.	Zea mays.	Ms45; male; plant tissue	Zea mays Ms4	08-JUN-1999	AAX07408;	RESULT 1 AAX07408 ID AAX07408 star
WPI; 1999-105628/09. New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.	(PION-) PIONEER HI-ERED INT INC. Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;	97US-00880499.	98WO-US012895.				M845; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; maize; hybrid seed; fertility; ss.	Zea mays Ms45 male tissue-preferred regulatory region.	(first entry)		T 1 408 AAX07408 standard; DNA; 1394 BP.

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                     The sequence is that encoding an M845 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably M845), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
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Query Match
Best Local Similarity
Matches 1311; Conserv

100.0%; ilarity 100.0%; Conservative 0

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Score 1311; DB 2; Pred. No. 1.2e-269; Mismatches

DB 2;

Length 1394; Indels

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Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T;

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XPXA	•	ACTTTTGTGTA 3	63 63
RESUL AAH76 ID XX	•	241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300	N N
Db	,	181 CTGACCGAGGCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	ш п
Q Db		121 CTCCATGITCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTGCTAT 180 	р р
Q Db		61 CTTCTTCTGCCTTATTACTGACTGAATGGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	
Q D		1 CCATGGTGTCTCTATGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	
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                                                                                                                                                                 1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGCCATACTACATGCTTGTTCAACCGTTCGTC
                                                                                                                                                                                                                                                                                  1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCCTACGTCA 1140
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ccarcrracrcarecaacrrccarecaacacacacacararerrrccreaac 1311
                             CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                  TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT
                                                                                                           TYGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260
                                                                                                                                                                                                    GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200
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LT 3 6332 AAH76332 standard; DNA; 1394 BP. Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds. Z. mays Ms45 male tissue-preferred regulatory region encoding DNA. 29-OCT-2001 (first entry) AAH76332; Zea mays.

WO200160997-A2

23-AUG-2001.

13-FEB-2001; 2001WO-US004527

15-FEB-2000; 2000US-00504487.

(PION-) PIONEER HI-BRED INT INC.

Albertsen MC, Fox TW, Garnaat CW, Huffman G,

WPI; 2001-514772/56.

Claim 4; Page 46; 50pp; English.

A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene inpacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from 2. mays

Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;

uery Match 100.0%; Score 1311; DB 5; est Local Similarity 100.0%; Pred. No. 1.2e-269; atches 1311; Conservative 0; Mismatches 0; CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC Length 1394; 0 Gaps

61

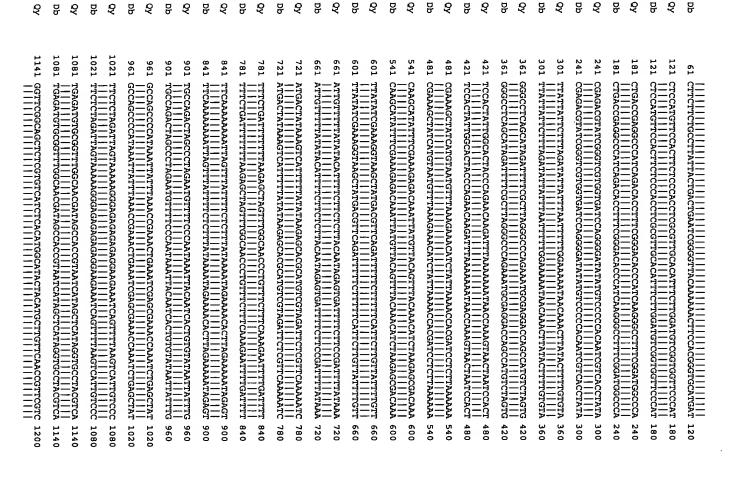
CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120

CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC

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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 1311;
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 matissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001; 2001WO-US004527
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 mays Ms45 male tissue-preferred regulatory region

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH76333
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1394 BP; 411 A; 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hybrid seed; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC
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                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
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                                                                                                                                                                                                                                                                                                                             Score 1311; DB 5;
Pred. No. 1.2e-269;
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AAH76334 standard; DNA; 158 BP. XX AC AAH76334;		1201 TIGTICCATGGTCCAAGCCTIGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260
		1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTGGCCAGCTCGTCGTCGTCACACACA
1265		
OY 1205 TCCATCGTCCAAGCCTTGCCTAT		
Matches 163; 1145 CC		
Sequence 255 BP; 59 A; 86 C; Query Match Best Local Similarity 97.6%;	,	
impacts male tertility of the exogenous gene. A method of present sequence represents a		841 TICAAAAAAATTAGTITATTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900
rodi	-	781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC
Example 5; Fig 8; 50pp; The invention provides a		721 ATGACTATAAAGTCATTTTTATATAAAGACAGCATGTCGTAGATTCTCGTTCAAAAAAC 780
AA PT A male tissue-preferred regulator PT essential for initiating transcri PT mediating fertility in a male pla		
PI Albertsen MC, Fox TW, Garnaat C XX DR WPI; 2001-514772/56.		
PR 15-FEB-2000; 2000US-00504487. XX PA (PION-) PIONEER HI-BRED INT INC.		
PD 23-AUG-2001. XX PF 13-FEB-2001; 2001WO-US004527. XX		481 CGAAAGCTATCATGTAATGTTTAAAGAACATCTTTTAAAGCAGGATCCTCTTAAAAAA 540
OS Zea mays. XX PN WO200160997-A2.		
issue; reg		
	- 33	
RESUL AAH76 ID XX		
Db		181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240
Qy 1261 CCATCTTACTCATGCAACTTCCATG		

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                                                                                                                                     rred regulatory region comprising nucleotide sequences ating transcription of the MS45 gene useful for in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory region; transcription; male fertility; er; ds.
                                                                  rative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TW, Garnaat CW, Huffman G, Kendall TL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   er fragment.
caactrccargcaaacacgcacatatgrtrcctgaac 171
                      Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -US004527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NA; 255 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00504487.
                                                                                                                                                                                                                                                                             A; 86 C; 39 G; 71 T; 0 U; 0 Other;
                                                                                                                                                                                                                           12.3%;
                                                                                                                                                                                                        Score 160.6; DB 5; Length 255; Pred. No. 1.5e-24; 0; Mismatches 4; Indels 0.
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays MS45 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514772/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M845; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2001
plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                    Plant full length insert polynucleotide segid 23340.
                                                                                                             ADX48600;
                                                                                                                                      ADX48600 standard; cDNA; 320
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                     1155 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC-TTGTTCCATCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M845 male
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                                                                                                                                                                                                                                                                                  CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                          GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                            GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                                                                                 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                                                                                                                                                     CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTTGTTCCATCGTC
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 41 A; 50 C;
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                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fox TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue-preferred
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                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                         Score 146; DB Pred. No. 1.7e O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regulatory region fragment.
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.7e-21;
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                                                                                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                   Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC polynucleotide consisting of a sequence encoding an amino acid sequence content of the sequence at available in electronic form from the US patent office at the pseudata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as construct is useful for configuration of the recombinant DNA construct is useful for common to conditions, pathogens or pests, for manipulating growth rate in colls by modification of the cell cycle pathway, for conferring confirmed the plant disease, for producing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert of the construct of the 
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05-NOV-2001; 2001US-00985678
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TABASKA J E.
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GCCCTTAATT 191
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RESULT 8
ADX33444
                                                                                         The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence conditions are also useful form from the US patent office at the sequence introduced are consistent of the superior conference than 1700-013-2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as construction are also useful in physical arrays of molecules and as construction of the invention are also useful in physical arrays of molecules and as construction of the conditions, pathogens or pests, for manipulating growth rate in commodification of the cell cycle pathway, for conferring concreased resistance to plant disease, for producing galactomanan, in construction of the cell cycle pathway, for conferring concreasing the rate of homologous concreased resistance to plant disease, for producing galactomanan, construction of the condition of the cell cycle pathway, for conferring construction of the construction of the cell cycle pathway. For conferring construction of the cell cycle pathway, for conferring construction of the cell cycle pathway. For conferring construction of the cell cycle pathway, for conferring construction of the cell cycle pathway. For conferring construction of the cell cycle pathway, for conferring construction of the cell cycle pathway. For conferring construction of the cycle pathway, for conferring content. This sequence represents a plant full length insert construct of the cycle pathway cy
Query Match
Best Local S
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(ZHOU/) ZHOU Y.
(KOVA/) KOVALIC D K.
(SCRE/) SCREEN S E.
(TABA/) TABASKA J E.
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05-NOV-2001; 2001US-00985678.
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                                                                                         Sequence 624.
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     Score 74; DB 13;
Pred. No. 5.4e-06;
0; Mismatches 35
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of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, harbicides, extreme comotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide for the polynucleotide for

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plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; hat tolerance; drught tolerance; hetbicide tolerance extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lighin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; yield; plant growth; plant development;
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protein content; gene; ss
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05-NOV-2001; 2001US-00985678.
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ZHOU Y.
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tolerance; herbicide tolerance;
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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2445 BP;
  Claim 1; SEQ ID NO 17816; 15pp; English
                                                                             cold, heat,
pests, for c
                                                                                                                                                                                                                                                                                                                                        (KOVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant full length insert polynucleotide segid 17816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADX34996 standard; cDNA; 928
                                                                                                                                                                                                                                                                                                                                                                                        (/noHZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001;
                                                  improving
                                                                                                                                                                                                                                                                                        (CAOY/)
                                                                        recombinant DNA construct, useful for improving plant tolerance to d, heat, drought, herbicides, extreme osmotic conditions, pathogens or to, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                     ٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1683
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                                                                                                                                                                                                                                                                                                             ZHOU Y.

KOVALIC D K.

SCREEN S E.

TABASKA J E.
                                                                                                                                                                                                                                                                                        CAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                     Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTAAGAGCTAGTTTGGCAACCCTGTTTCTT-TCAAAGAATTTTGATTTTTTCAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTAGGGCTAGTTTGAGAACCCCTTTTTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCTTAATGTTTTTTTTCATGAA 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00304517.
2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                     Kovalic
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Pred. No. 1
                                                                                                                                                                                                                                        Screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                     SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        796 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                     Tabaska JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc polynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide cf the seqdata.uspto.gov/sequence.html?DocID:2014034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as improving plant tolerance to cold, heat, drought, herbicides, extreme combinit conditions, pathogens or pests, for manipulating growth rate in collant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, cc lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake cor by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert to fithe collynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombinant was conscious, for drought tolerance; herbicide tolerance cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; galactomannan production; lignin production; plant growth regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 928 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at
(LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant protectant; plant growth regulant;
                                                                                                                                                           06-MAY-1999;
05-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                            US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant full length insert polynucleotide seqid 31957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant growth; plant development; n content; gene; ss.
                                  ZHOU Y.
KOVALIC D
      SCREEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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2001US-00985678
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78.0%;
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Pred. No. 1
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L.8e-05;
hes 27;
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RESULT 12
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recombination in plants, for improving yield by modification of photosynthesis or plant growth are plant of the recombinant DNA construct under the photosynthesis or by providing improved plant to plants, for improving plant to examine the plant of the conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, light or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of the cell cycle pathway, for conferring light or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of recombination or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represente a plant full length insert content. This sequence representes a plant full length insert in plants of the plant can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or peets, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 31957; 15pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TABA/)
(CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-180133/17.
                                                                                                                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
              Unidentified
                                                                  extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomanan production; lignin production; plant growth reguiyield; plant growth; plant development; seed oil; protein yield
                                                                                                                                                                                                          Plant full length insert polynucleotide seqid 31061.
                                                                                                                                                                                                                                               21-APR-2005
                                                                                                                                                                                                                                                                                 ADX60218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mproving yield
                                                                                                                                                                                                                                                                                                                    ADX60218 standard; cDNA; 3607
                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1858
                                                                                                                                                                                                                                                                                                                                                                                                             1918
                                                                                                                                                                                                                                                                                                                                                                                                                                              912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhou Y, Kovalic
                                                  plant growth;
n content; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C¥
O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTTAGAAAAATAGAGTTGCCAGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                           CCCTTAATGTTTTTTTCATGAA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 685 A; 484 C; 524 G; 844 T; 0 U; 0 Other;
                                                  gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.5%;
                                                      88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71.8; DB
Pred. No. 2.2e-(
0; Mismatches
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                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
2.2e-05;
nes 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tabaska JE,
                                                                     plant growth regulator;
oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao
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RESULT 13
AAL15210/c
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                                                                                                                                                                                                                                     문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Sim
Matches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osmotic conditions, pathogens or pests, for manipulating growth rate in osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a recombinant DNA construct comprising polymucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at ftp. seadata.uspto.gov/sequence.html?DocID:2004034888. The polyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-FEB-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions. nathogeness of particular and particular arrays of molecules and as plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions. nathogeness of particular arrays of the province of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 31061; 15pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-180133/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or by providing improved plant growth and development under at least stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polymucleotide that can be used in the recombinant DNA construct of
07-DEC-2001
                                                    AAL15210;
                                                                                                  AAL15210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TABA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (/nohz
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TABASKA J E
CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KOVALIC D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                CCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                                                                                                                                                                                                                  TTAGTTTATTTTCTCTTTATAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAGACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTCAAAGAAAAA
                                                                                                        standard;
                                                                                                                                                                                                                                        CCCTTAATGTŤTŤTTTCAŤGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.5%;
milarity 73.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 915 A; 695 C; 718 G; 1279 T; 0 U; 0 Other;
      (first
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                                                                                                           cDNA;
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                                                                                                           883
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Pred. No. 2.4e-
0; Mismatches
                                                                                                           В₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  construct of the
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cancer expressed polynucleotide 7667.

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Best Local
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29-MAR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polymerically preventing breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-2000;
14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides are also useful for isolating activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200151628-A2
                                                                                                                                                                                                                                                                                                                                                                                               237;
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513
                          779
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                                                                                                            633
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                                                                                                                                                                                                                                                                                                                                                                 TGTCCACTATTGGCACTACCCAGAACAAGATTAAAAAAATAACCAAAGTAACTAATCCA
AAAAAAATTTTTTNAAANTNTTTTTAAAAACCTTNAATTNAAANANAATTTTTTTNNNTT
                    AAAAAANNTTTTTTTTTTTATANTTTATAAAAAATTTTATTTNTNTTTTTCTNAAAANA
                                                                                AAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAA
                                                                                                            TTATTGTTTTATATACATTTTCTTCTTCTTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                                                                                                                                                            AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTG
                                                                                                                                                                                                                        TTAAANNTTTNTAANTTATTÄAACCAAAATTTTTTTTÄÄÄÄÄÄÄÄÄTTTTTÄAAANTT
                                                                                                                                                                                                                                                    AACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACA
                                                                                                                                                                                                                                                                                TANAAATTTTTTTNAAAAACTAATTNTAANNATANTNAATTTTTTNTAAAAAAANNNAAAAA
                                                                                                                                                                                                                                                                                                         CTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAA
                                                                                                                                                                                                                                                                                                                                      TGTTNANNNANACCTANACCTTTAAANATNTNNANTTNAANNAAAAAAATATTTAAANN
                                                                                                                                                                    <u>AATAANTTNAATTTTTTTTTAATNAAAAAAAAAATTTNAAATTTTAANCAANTNTTTTTT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0176077P.
2000US-0189167P.
2000US-0192099P.
2000US-0193480P.
2000US-0205230P.
2000US-0221315P.
2000US-0220534P.
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 322 A; 18 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          5.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell marker; cytostatic; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70.2; DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.8e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 G; 396 T; 0 U; 124 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 883
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Best Local Similarity Matches 237; Conserv

Conservative

0,

Mismatches

Indels Length

<u>,</u>

5.4%; 39.2%;

Score 70.2; DB 11; Pred. No. 3.9e-05;

Query Match Best Local

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RESULT 14
ACN85231/c
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                     The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequence given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=2003009974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACN85231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast cancer related marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACN85231
Sequence
                                                                                                                                                                                                                                                           Novel isolated polypeptide associated with breast cancer, detecting presence of polypeptide in sample, as a marker i
                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2001; 2001US-0306220P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003099974-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer; breast;
                                                                                                                                                                                                                  Disclosure; SEQ ID NO 6381; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2002; 2002US-00198846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1019
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flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds.
Danilevskaya O, Hermon P, Bruggemann E, Shirbroun D,
Rafalski JA, Sakai H, Cahoon E, Cahoon R, Klein T;
                                                                                                                         30-JAN-2003; 2003US-00343477.
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                                                                                                                                                                                                             12-AUG-2004
                                                                                                                                                                                                                                                                                            Zea mays.
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WPI; 2004-580996/56.

New polynucleotides, specifi flowering locus T gene (FT) homologs, useful for floral specifically nucleic acid fragments encoding ne (FT) or terminal flower' (TFL), or Apetala3 (Ap3) floral development, e.g. engineering plant flowering

Claim 6; SEQ ID NO 63; 109pp; English.

CC The present invention describes an isolated polynucleotide comprising a CC first, second, third, fourth or fifth nuclectide sequence, or their complement encoding a polypeptide either having flowering locus T gene (FT), terminal flower (TFL), or Apetala (Ap3) homologue activity. Also CC described: (1) a vector comprising the polynucleotide; (2) a recombinant CC DNA construct; (5) producing a plant comprising the polynucleotide; (3) transforming a cell by crecombinant DNA construct; (5) producing a plant comprising three comprising three comprising transforming a plant cell with the polynucleotide; (4) a cell comprising the construct; (7) a seed comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (8) an accombinant DNA construct; (9) an isolated polynucleotide sequence comprising a first nucleotide sequence, where the first nucleotide sequence is comprised by another polynucleotide, where the comprised the second, third, fourth, fifth or six nucleotide sequence; (9) an isolated polypeptide having FT or Ap3 construct; (9) an elected above; and (10) isolating a polypeptide cell containing a recombinant DNA construct; comprising the polypeptide from a cell containing a recombinant by another polynucleotide sequence; (9) an isolated polypeptide having FT or Ap3 containing a recombinant by another polynucleotide for a sequence comprising isolating the polypeptide from a cell containing a recombinant by another polynucleotide sequence cell containing a recombinant by another polynucleotide sequence appears the polynucleotide sequence appears the polynucleotide sequence are useful cfor first pulme, plant growth rate, inflorescence architecture, and tissue culture morphology and the rate of cell division to enhance cransformation. The present sequence represents an FT homologue

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Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;

Query Match Best Local Sim Matches 89; Similarity 73.6%; Conservative 0; Mismatches Score 69.8; DB 13; Length 13400; Pred, No. 9e-05; 32; Indels <u>,</u>

밁 S 8619 AAAAATAAAAATCCATTAGAAAATGGGGTTGTCAAACTAGTCCTTATTTAGTTTTCCAT 8678 871 TAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTTCCCAA 930 931 T 931

8559 ACCATTTTATTTTCAAGAGGTTTTTTATTTTATCAAGAAAATTAGTTCATTTTCTCTTGG 8618

811 ACCCTGTTTCTACAAGAATTTTGATTTTTCAAAAAAATTAGTTTATTTTCTCTTTA 870

밁 8679 T 8679 В

Search completed: March Job time: 875.437 secs **ω** 2006, 18:11:32

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Sequence:

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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AUTHORS
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JOURNAL
                 Query Match 100.0%; Score 1311; DB 6; Best Local Similarity 100.0%; Pred. No. 7.2e-228; Matches 1311; Conservative 0; Mismatches 0;
                                                                                                                                                                                  PF 19-JUN-1998 JP 1999504910
PF 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFWAN, PI TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC
,COTKL4/34, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC
CC Strandedness: Single;
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PD 30-OCT-2001
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Male tissue-preferred regulatory region and method of using same.
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1 (bases 1 to 1394)

Alberreen,M.C., Pox,T.W., Garnaat,C.W., Huffman,G.A. and Kendall,T.L.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                     GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT
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Matches 1311; Conser
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Albertsen, M.C., Fox, T.W., Garnaat, C.W.,
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OY 481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540 Db 481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAAACCACGATCCTCTTAAAAAAA 540	AACCGTTCGTC 1200 AACCGTTCGTC 1200	1141 GGTTCGGCAGCTCTCGTCTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGT
Qy 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAATAACCAAAGTAACTAATCCACT 480 Db 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480	TGCCTACGTCA 1140	1081 TGAGATGTGCGGTTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA
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Qy 121 CTCCATGTTCCACTTCTCCCACCTGGGGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	ATTTTGATTTT 840 ATTTTGATTTT 840	781 TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC
Qy 61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	TTTCAAAAATC 780	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC
Qy 1 CCATGGTGTCTCTATGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	TTTTCTTCCGATTTTATAAA 720 TTTCTTCCGATTTTATAAA 720	661 ATTGTTTTTATACATTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA
Query Match 100.0%; Score 1311; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 7.2e-228; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TTATTTTGTT 660 TTATTTTGTT 660	601 TTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTCATTCTTGTTATTTTGTT
/mol type="unassigned DNA" /mol type="unassigned DNA" /db_xref="taxon:4577" ORIGIN	\GAGCGACAAA 600 \GAGCGACAAA 600	541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAA
6	TCTTAAAAAA 540 TCTTAAAAAA 540	481 CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA
- X	CTAATCCACT 480	421 TCCACTATTGGCACTACCCAGAACAAGATTAAAAAAATAACCAAAGTAACTAATCCACT
ORGANISM Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	ATGTCTAGTG 420 ATGTCTAGTG 420	361 GGGCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG
1 GI:155546	CTTTTGTGTA 360	301 TTATTATTCTTTAGATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGGTA
AX224394 AX224394 1394 bp DNA linear PAT 10-SEP-2001 DEPINITION Sequence 1 from Patent W00160997.	GTCACCTATA 300	241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA: 3.00.5.5

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Query Best 1 Match	JOURNAL JOURNAL FEATURES SOUR	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 4 AX224395 LOCUS DEFINITION	B 6	B &	B 8	문왕	Db Qq	P &	Db 69	유 성	g &	Db Qy	Db
Query Match 100.0%; Score 1311; DB 6; Length 1394; Best Local Similarity 100.0%; Pred. No. 7.2e-228; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	PAGE LEBUS PROFESSION TO THE PROFESSION TO THE PROFESSION TO PROFESSION TO THE PROFESSION THE PROFESSION TO THE PROFESSION TO THE PROFESSION TO THE PROFESSI		AX224395.1 GI:15554637 Zea mays Zea mays Zea mays Zea mays	AX224395 1394 bp DNA linear PAT 10-SEP-2001 Sequence 2 from Patent WO0160997.	1261 CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311	1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260 	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200	1081 TGAGATGTGCGGTTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140 	1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGGAAGAAATCAGTTTTAAGTCATTGTCCC 1080 	961 GCCAGCCCCATAAATTATTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 	901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTT 960 	841 TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900 	781 TITCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTT 840	721 ATGACTATANAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780	661 ATTGTTTTATATACATTTTCTTCTTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 720
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ORIGIN ORIGIN ORIGIN OUETY MATCH OUETY MATCH DEBUT Local Similarity 100.0%; Score 1311; DB 15; Length 3343; Best Local Similarity 100.0%; Pred. No. 6.2e-228; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OF CONTROL OF THE CONTROL OF T		/gene="Ms45" /product="ms join(1392. /gene="Ms45" /codon_start" /product="ms	/db_ref="taxon:4577" /db_ref="taxon:4577" /chromosome="9L" /chromosome="9L	62nd Ave., F.O	AUTHORS FOX, T.W. Trimnell, M.R. and Albertsen, M.C. TITLE Cloning of Me45, a gene required for male ferility from Zea mays JOURNAL Unpublished REFERENCE 2 (bases 1 to 3343) RUPHORS FOX, T.W., Trimnell, M.R. and Albertsen, M.C. TITLE Direct Submission JOURNAL Submitted (13-MAR-2001) Trait and Technology Development, Pioneer	AF3 Zea Zea Euk Spe cla	RESULT 5 AP360356 AP360356 AP360356 DEFINITION Zea mays male fertility protein (Ms45) gene, complete cds. ACCESSION AP360356	1201 1261 1261	Db .1081 TGAGATGTGCGATTTGGCAACGATAGCCACGTAATCATAGGTGCCTACGTCA 1140 Oy
Qy 1021 TTCTCTAGATTAGTAAAAGGAAGAAGAAGAAATCAGTTTTAAGTCATTGTCCC 1080	OY 901 TGCCAGACTAGCCCTAGAATGTTTCCCCAATAAATTACAATGACTAGTATAATTAGTTG 960 901 TGCCAGACTAGCCCTAGAATGTTTCCCCAATAAATTACAATGACTAGTATAATTATTTG 960 901 TGCCAGACTAGCCCTAGAATGTTTCCCCAATAAATTACAATCACTGTGTATAATTATTTG 960 901 TGCCAGACCCCATAAATTAATTAAACCGAAACTGAAATCACTGAGAAACCAAATCTGAGCTAT 1020 961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020	781 TTTCTGA 781 TTCTGA	Db 661 ATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTCCGATTTTATAAA 720 Qy 721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780	TRATATOGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTTTTTGTT	Qy 481 CGAAAGCTATCATGTAAATGTTTAAAGAAACATCTATTAAAACACGACGATCCTCTTAAAAAA 540	Db 361 GGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCCAAAGTAACTAATCCACT 480 Qy 421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAAAA	301 TTATTATTCTTTAGATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTA	181 181 241	Qy 61 CTTCTTCTGCCTTATTACTGACTGATGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                    HI-BRED INTERNATIONAL,
Location/Qualifiers
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/mol_type="unassigned
/db_xref="taxon:4577"
   /organism≕"Zea mays"
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                                                                                                              Fox, T.W.,
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Pred. No. 4.5e-19;
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a
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Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H.,
Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
Quackenbush,J.
Consortium for Maize Genomics - BAC skim sequencing and assembly
                                                                                                                                                                                                                      Submitted (25-JAN-2005) The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850 On Jan 25, 2005 this sequence version replaced gi:57863105.
                                                                                                                                                                                                                                                                                                                 Submitted (15-JAN-2005) The Institute for Genomic Research (TI 9712 Medical Center Dr. Rockville, MD 20850
3 (Dases 1 to 188283)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanhiguel, P., Ma, J., Pontaroli, A.C., Rohling, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a
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HTG; HTGS_PHASE1.
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTTGTTCCATCGTC
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                                                                                                                                                            Center name: TIGR Seq_lib_id: ZGFX
                                                                                                           Web site: http://www.tigr.org/tdb/tgi/maize/Contact: maize@tigr.org
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/db_xref="taxon:4577"
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Pred. No. 2.2e-16;
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and

and

/estimated_length=unknown	1	gap 142805142904	gap 134045. 134144	gap 126465126564	/estimated_length=unknown	/estimate	gap 104000104099	gap 9867698775	/estima	gan 9650296601		gap Siter Sizer Gap Ga	/estima	gap 27965 28064		/clonea"ZMMBBC0196114"	୯ ପ ।	/mol_type="genomic_DNA"	rce 1	Location/Qualifiers	 184424 184523: gap of unknown Length 184524 188283: contig of 3760 bp in length 	184423: contig of 11079	173244:	605: gap of unknown length	 167406 167505: gap of unknown length 167506 171505: contig of 4000 bp in length 	167405: contig of 5220	162085: contig of 1009	* 15981/ 1609/6: Concig of itso up in rengen	159816: gap of unknown	 154521 154620: gap of unknown length 154621 159716: contig of 5096 bp in length 	2905 154520: contig of 11616	142804: contig of 8660	5 134044: contig of 7480 5 134144: gap of unknown	* 123578 126464: contig of 2887 bp in length * 126465 126564: gap of unknown length	478 123577: gap of unknown]	0 104099: gap of unknown length	* 98776 103999: contig of 5224 bp in length	98675: contig of 2074	96501: contig of 46647	49854: gap of unknown]	* 35161 35260: gap of unknown Length * 35261 49754: contin of 14494 bp in length	5160: contig of 7096	2/964: concig of syst	22233: gap of unknown length	conti	 This record will be updated with the finished sequence as soon as it is available and the accession number will 	,	
TITLE													AUTHORS	REFERENCE	JOURNA		AUTHORS			ORGANISM	SOURCE	VERSION	ACCESSION	DEFINITION	TOCUS	RESULT 9		: Db	γQγ	50		- -	Db	Qy	Matches	. Query Match		ORIGIN	gap	gap	Gab		. gap	gap	1. 3rd	The state of the s	.	
Direct Submission	Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.	Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Y.	Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer.B. Stange-Thomann,N., Stojanovic,N., Stubbs,M.,	Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,	Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,	Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,	Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,	Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,	Y. Graham, L., Grand-Pierre, N., Halez, N., Hagopian, D., Hagos, B., Hallar, J., Haller, T., Johnson, R., Jones, C.,	Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,	<pre>Diaz.J.S. Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,</pre>	Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,	Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,	2 (bases 1	Zea mays, cione zmmbscussaaui Ni Unpublished	and Messing, J.	RS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.	clade; Panicoic	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD	Zea ma	Zea mays	AC147602.5 GI:51315585	AC147602	Zea may	AC147602 186199 bp DNA linear HTG 17-AU			35630 TAGCCCTA 35637	909 TAGCCCTA 916			849 AAATTAGTTTATTTTCTCTTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGAC 908	35512 TTGTTTAAGGGCTAGTTTAAGGACCCTGTTTTTAAAGGGGATTTTTATTTTCTTAAGAG 35569	789 TITTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTCAAAAA 848	103; Conservative . C	al Similarity 80.5%; Score //.2; US		/6	18			/estimated length=unknown			/6	159717159816 /estimated length=unknown 160977 151976		

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 manually curated. It is the best representation of the BAC that we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bharti, AK and Messing, J: The Plant Genome Initiative at Univers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)

Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 17, 2004 this sequence version replaced gi:49658659. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- Project Information
                                                                                                                                                                                                                                                                                                                 consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
by the finished sequence as soon as it is available and the accession number will be preserved.

1 100617: contig of 100617 bp in length
100618 100717: gap of unknown length
100718 104730: contig of 4013 bp in length
                                                                                                                                                                                                                        provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 186199)
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Center clone name: 334_A_1
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Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
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REFERENCE
AUTHORS
TITLE
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CR936840
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KEYWORDS
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Best Local
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                                                                                                          Submitted (24-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquirities: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 26, 2005 this sequence version replaced gi:60279457.
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                   CR936840 161616 bp
Danio rerio clone DKEY-91021, ***
                  Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
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                                                                                                                                                                                                                                                                                                           Danio rerio
                                                                                                                                                                                                                                                                                                                            HTG; HTGS PHASE1.
Danio rerio (zebrafish)
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Center project name: zK9102:
                                                    Web site:
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100618. .100717
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/cultivar="B73"
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115104: contig of 10274 bp in length
115204: gap of unknown length
156396: contig of 41192 bp in length
156396: gap of unknown length
179396: contig of 23440 bp in length
180036: gap of unknown length
186199: contig of 6163 bp in length.
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Insert size: 160313; 4.7% error; agarose-fp
Quality coverage: 6.55x in Q20 bases; sum-of-contigs Quality
coverage: 6.56x in Q20 bases; agarose-fp
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Consensus quality: 156361 bases at least Q40
Consensus quality: 157330 bases at least Q30
Consensus quality: 158179 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ssembly program:
                                                                                                                                                                                                               fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Danio rerio"

ol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:01299 ragment_chain:1"
note="assembly_fragment:00794
                                                         note="assembly_fragment:00463 ragment_chain:1"
                                                                                                                note="assembly fragment:00606 ragment_chain:1" 6828. .79067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_fragment:00020
ragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db xref="taxon:7955"
;lone="DKEY-91021"
lone lib-">-
                                                                                                                                                                                                                                       note="assembly_fragment:00002
ragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_fragment:00342
ragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ote="assembly_fragment:00240
agment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3158: contig of 3158 bp in length 3258: gap of 100 bp. 11860: contig of 8602 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XGAP4; version 4.5
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contig
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of 100 bp
tig of 2726 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ig of 2237
of 100 bp
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of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 9840 bp in length 100 bp of 23134 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18226 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24523 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2237 bp in length
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AUTHORS
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AC117267
LOCUS
DEFINITION
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VERSION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79191 TTATAAAATNNNNAANAAAAAAAAAAATATATAAAATTTTTNNTANNTTNNATTTAAT 79250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79551 ATATATATATATATATTTTTT 79574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     936 TACAATCACTGTGTATAATTATTT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 TAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCAATAAAT 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           816 GTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAAATTAGTTTATTTTTCTCTTTTATAAAA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   696 AGTGATTTTCTTCCGATTTTATAAAATGACTATAAAAGTCATTTTTATATAAGAGCACGCA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 TTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25769 bp libityostelium discoideum chromosome AX4, complete sequence.
AC117267 AC115507
                                                                                                                                                                                                                                          (Dases 1 to 25789)

1 (bases 1 to 25789)

2 (bases 1 to 25789)

3 (bases 1 to 25789)

4 (bases 1 to 25789)

4 (bases 1 to 25789)

4 (bases 1 to 25789)

5 (bases 1 to 25789)

6 (bases 1 to 25789)

7 
                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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                                                                    The Dictyostelium Genome Sequencing Consortium (2 (bases 1 to 25769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                     ce and analysis of chromosome 2 of Dictyostelium discoideum 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment_chain:1"
97494. .103542
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fragment_chain:1"
[58891._161616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment:00044.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="assembly_fragment:00074
ragment_chain:1"
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37399. .158790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:42733680
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Pred. No. 0.00071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rTTTTTTATATTTTATTATTATTTTTTATTTTTAATAT. 79310
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:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear INV 21-FEB-2004
2 2 map 5836255-5862024 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 161616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTTTTTTNTA 79490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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FEATURES

source

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REFERENCE
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TITLE
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On or before Feb 21, 2004 this sequence version replaced
gi:19570016, gi:20087114.
CDS predictions from GeneID may contain errors. Further Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (09-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany (bases 1 to 25769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-FEB-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baumgart, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agency: Deutsche Forschungsgemeinschaft (DFG).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OHIERVKORDDVPIIIVGNKVDLESRRQVSRIEADQLARSLRVPYIETSAKTRSNIEE
AFFTLVRHTPRNITYYKVVWGGGGVGKSAIIIOPIQNHFVEEYDFIIEDSYRKQVTIS
GLPPIGGSLMKKGSSGSSSSSSSSKRGLFMLIFSGKUKQBSPQQAASPSTIDRTGQI
STNRLEANVLSYSMSNLSKEVPLITGDCVYCQGCNVILSRFSNLVKTGDDSFTWKCEF
CKYSNSNILLEQGEIPNKDSVEYVLSSPSTSSTTDGSKREESIIIYCIDVSGSMGITT
EVPSLQSEWNAKKGVKGASSGPSYISRLECVQSSIPFIDBLSIQVSKRAKVULVTFS
EVPSLQSEWNAKKGVKGASSGPSYISRLECVQSSIPFIKAKVULVTFS
DEVMIYTQSNSVDGPIVLAGDKLEDPDQLIEIGRSMTYDKLPTASGSSDFLKAKIKSL
EPVQSTALGPALLVSAAIASQKMLSEVVICTDGVBNVGLGAIEDLFAGPAGEFYEKVT
KLAQNNKTTINIIGISGSHIDLGVIGKVSEQTNGNITTIHPLELAREIEKLTQNPMIA
TDVEMSICLHFTLEINKYDSKQGLSRVVKQFPBNNSLTDLTLLYSSRNRFTEFVQIYP
FQIQIKTKLDGVRCLEVVSAQLQATDBNTSTSNANISILANAFTQQAKKLAQQGEY
FGILHVANGVIDEGUEGNTSTSNANISILANAFTQQAKKLAQQGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
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/translation="MRLQIILFLSILLIFQLKSTFSSNDISSTILSITPNFNKDYNNQ
/translation="MRLQIILFLSILLIFQLKSTFSSNDISSTILSITPNFNKDYNNQ
ILSKSEWFRSLEYSSNKKVIFBVFDGFNHEYIENLDRIIKEREHKVYGVDFSFSCFCL
NSKFNYLEVIKKFSTISRNNKYFENIMLNISSTHENCYLSYNISNYLYNKNNNEYQEFUN
FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENIMLNEKSSLFFFYLKNIANNQEFEDYY
FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENIMLOKSSSNNNNNNNNNVDDETLTLLGSGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="GeneID exon scores (in order of location ranges):
24.88, 254.96 - GSCJ_ID dd_00753"
/codon start=1
/product="hypothetical protein"
/protein id="AAS38626.1"
/db_xref="GI:42733682"
/translation="MEPFTKYVYITSNLDKPKEWFTQSEMSLTTTTDTIQKSFVNNSG
SSSSSKGFGEAVILDILDTAGQEEYSAMRDQYVRTGDCFMIVFSIDSRSSFEEYSQLK
SSSSSKGFGEAVILDILDTAGQEEYSAMRDQYVRTGDCFMIVFSIDSRSSFEEYSQLK
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GTITTTSGGNNNNNSTSPSTNPVSFDRVVDHSNNNQIQIVIDSFVNINNNNNNNN
KENNNNNYXPDPSTTEMTITTIJKSCTLEQIGTIGDDCYSTNTTPBSPTSSSSSTSSLLNN
KENNNNNYXPDPSTTEMTITTIJKSCTLEQIGTIGDDCYSTNTTPBSPTSSSSSTSSLLNN
KNNHWMMPSIKINQIINNNNNNNNNNNNNNNNNNNNNNNNNNTPBSPTSSSSCSPIEDEHIQE
                                                                                                                                                                        Hypothetical protein"
/protein_id="AAS38627.1"
/db_xref="GI:42733683"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MESRLHLKAATKLIRSLCNTDEQWEEFYNFEVLRBEMEAPLITCIKNKQQRVEKAATD
DEIQVFYKMKNVHKSFVEGGRKKDISRRKGEAEINKQYYNIKFT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSGSGSSGTSGAQLSGTGYVINHQ"
join(2957. .3173,3272. .5583)
                                                                                                                                                                                                                                                                                                                              /note="GeneID exon scores (in order of location ranges):
68.61 - GSCJ_ID dd_00752"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5711. .6796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="GeneID exon scores (in order of location ranges):
23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="5836255-5862024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="genomic DNA"
strain="AX4"
                                                                                                                                              translation="MSSRVKSLIERYNGINLTIEKSLSPRGLINTNINNNINNNNNNNN
                                                                                                                                                                                                                                                                                               /product="similar to Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .25769
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                                                                                                                                                                                                                                                                                        falciparum (isolate 3D7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sgo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gg
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/product="Binilia to protein SP87 precursor (PL3 protein)"
mold). Spore coat protein SP87 precursor (PL3 protein)"
/protein_id="AAS38631.1"
/db_xref="G1:42733687"
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/translation="MFIGEDCNKITNEEECHKSSECIVINYTPCCGEOKWACSKGTFD
/translation="MFIGEDCNKITNEEECHKSSECIVINYTPCCGEOKWACSKGTFD
/translation="MFIGEDCNKITNEECHKSSECIVINYTPCCGEOKSGGTSGGSSGGTSGSS
SGGSSGGVSSCGTTHCPEGYHCSMYNDDATCLASTTGGTGLPGTSSSTAGVSSCLTT
LCPIGHICVEDSNGVNCVPNGGGTSGGSSGTTSGGHPDPCNDVCPDGFHCEXDGK
TAKCVPSPTTGSSSTSGGHPDPCKDVTCPDGFHCECKDGKTAKCVPSPTTGSSSTSG
NTNPCSNVNCPDGFYCECKDGKTAKCVPSGTTQFPKPPCSLRCPPHHECRENDQHQ
CCVKVHHDRCSLRCPHGHECKVDHNGKECCVRSHRPPPPEVCSLRCPPHHECRENDQHG
KKCCVKLHCDBVCDLDCGGFBECKIHDGSKCCVRSHRPPPPEVCSLRCPPHECKFDDHG
KKCCVKLHCDBVCDLDCGGFBECKIHDGSKCCVRSHRPPPPDHEKCKNKCCPBGHECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLKNERINGNDGEITTTTTTTTTSRSSTTIMTTTTTMGVNIRMYLLFRQVWRNIVIK
TQILFHLRLYNIHANKKVFLTFIQL/DYKFKGYLQSMVLNYHDDNDDDADEDSYDSDI
DDDSYSDGGNGSSSGSSDGSSSNSINNGISSSSIILSNSSLLEISMIRVNSL
PEGLKSIEFEKEYNVIQDFLLPFSISSIFSYGFNORIKKGVISDNVISITFGDSFNQ
SLDGNWLFKQLKHLQFGHKFQQTIKMGQLPSSITSLILDPRSYKGVIEIGSIPDSVKT
LDYKFKSCSNOESISFNPIFKSITRLYFDSEENQNIKANDISSNYNLTSIHFGEHFNS
DIGIKSLPNSIRBIKFGRAFDRDIKLCPSSITS DFGNKFNRPLSMMTQTLTSIDFGS
KFNQIIPQGIFTHTKLKSLNFCYHFNQIIPADTLFPTLESLMLGGYNREITVKNDEYD
CYGISNKGGFGSNSSSNFCVGGTNNGLREMLKYTTSLKTLTLNYFNRKIEVGDLPNSI
ESLNLGYHFNQPIGNNYLFKLLKKLFILNSEFNQNISADGCIPFGLQTIYINSNMNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Juli 12884. .13020,13172. .15320)
(notee "GeneID exon scores (in order 2.42, 136.56 - GSCU_ID dd_00727"
/codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="similar to Dictyostelium discoideum (Slime mold). Hypothetical 97.7 kDa protein" (protein id="AAS38630.1" /protein id="AAS38630.1" /db_xref="GI:42733686" /tb_ni="MDNLIYDFLIKKEYNQQSFLDCILILSINGLYISYDGLLDYCNN FRLIENKTVNKEAISYYGLNYNQYQLLDEFTRLLKLKNKTTDCKNKIINTHNSLNKCC GRNKEDYSILIIIENNNNIINKDYQFKNNNKKSNNNIYNNNNNNNNNSIIEEKDLNKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
/product="hypothetical protein"
/protein id="AAS38629.1"
/db_xref="c1:4273862"
/translation="MEEKIKFYFEIIDFONOKFKIQEFTSKLIGLKEESFTTFKFIVY
/translation="MEEKIKFYFEIIDFONOKFKIQEFTSKLIGLKEESFTTFKFIVY
EKYLAWTQSIEESILKTNGYINKSIFEBIFSYCGYJGFFLEXEFTVFFTHKESFQIL
DDYLFEKINSLIMKLNEKEKLINGLIYYNNKMENKIGFFERSEINFONTHKESFGIL
DDYLFEKINSLIMKLNEKEKLINGLIYYNNKMENKIGFFERSSDASGDFILTISMIGIMDNYLI
INANSLWIKSSIDSRNISNSPINSRCSFNEYFEKRSSDASGDFILTISMIGIMDNYLI
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23.29 - GSCJ_ID dd_00728"
/codon_start=1
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LTDAPVAASSSSSVKYTIDVLLSFKSANTKRPIQIDIVENIQKEIVVPLSLPTTPYN
NINNNNNTNNSSQHNTANQGKYPIFSPOISPKKIAYAQSKTSTKTNINNNNNNNT
TKKANSNITTPGSNNENNHYNSNTKSSTKKONPIFSSLNTAFPNOKNTTTTESKKSTT
TTPKSNKKINDVNAAFAAVANSTTTTEQPVAIIDGATPSTNESPKKTPLKETDPKRLA
ARQRQIDIGKNTAAYKNYIALVPKSKRKPTDPKTPNKNQVCKKKSMDGQIKKMRRQLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein id="AAS38628.1"
/db.xref="GI:42733684"
/translation="MSSSTIITPIATTTNNNSSTNGIHNSKTNRTLFKNIKNNIPNS
pnnapikknsvgligngpnvnnnnkdrklnsnbgvnfgkknilettpsknsmysttkhs
pnnapikknsvgligngpnvnnnnkdrklnsnbgvnfgkknilettpsknsmysttkhs
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QNSMSPPKLDKRRFSRDLIPFTIANI"
Join(8924. 9076,9236. 10573)
/note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENSIIESKEFQTINYHAKSFFLLINDLYSFNREINENDLLNYIKILAIQLNSIQLSII
KTIBLIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNSNKILSGIYFAHKKSKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (10972. .11979)
VDQHGKECCVVAHR PPPKCSLRCPPRHECR VNHFGEECCVKVHHDKCSLRCPPGHECK
VDQHGKECCVVAHR PPPKCSLRCPPKHECR I NHFGEECCVKSRNDCLTCEDLNCERKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(16184. .16199,17272. .17613,17707. .19331)
/note="GeneID exon scores (in order of location
0.08, 32.32, 227.42 - GSCU_ID dd_00726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.37, 128.60 - GSCJ_ID dd_00729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="similar to Dictyostellum discoideum (Slime
mold). Spore coat protein SP87 precursor (PL3 protein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INSLUPLFITKYINIIDLSHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   order of location ranges):
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25-JAN-2005 IN PROGRESS

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RESULT 12
AC155379/c
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                     678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618 CTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTATATACAT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558 AGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 TGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACCAAGCATATTTCGAAAG 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 CCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAA 497
                                                                                                                                           858
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                                                                                                 TTATTTTTTTTTTTTTTTT 2829
                                                                                                                                                                                             TTTTTTTTTCAAACACCACCAATTTTTTTTTTTTTT
                                                                                                                                                                                                                                    TTAAAAATTGGGTGTTTGAATAAAATATTCTTTTAAATTTTTTCAGGAAATATCTTTT
                                                                                                                                                                                                                                                                                                                                      TTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAG
                                                                                                                                                                                                                                                                                                                                                                                        TTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATT
                                                                                                                                                TATTTCTCTTTATAAAAT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STYNNNNYYNVNNNSLANISNNADKNKKTITSTSATILNKENVELYNNGNNNLANKNS
EDILKOKSIKWNKVDGYITRTINFILLACNSMDLLSDESINYCOWSOCDFONVIEK
SLDERNQFAQLOVEVLARYEDDVWKKDYLNHLLETEGOSKIETKLKOQEGSKTVKNV
SCHIQFMSKLFSLIVYIPTYYTKYBRQNGSFSFFLNSQNGVISATRPEIGLGKIGDFLK
YTQNYESTLYGNEEPFEKCKDELAIIDSFKYYNTSSYFLTFSRSSTNFLGSSSIGHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DMYNDDDKSSTSSQSSSSSSSSSSSPKPIKNNDNNTTTYTTTATYTYTSKIATS
LSTIEKFQVFNVDQIPEISIEAYIERVFKYLPFGTDIFIFSTIYLDRLIQMQEIQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (21961. .24357)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KINPREGGNIYQSIKN"
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106.68 - GSCJ_ID dd_00725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCAMKTVPIDKENCCEKVPVCYSNNPLLDGGHGFI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="GeneID exon scores (in order of location ranges):
173.48 - GSCU_ID dd_00724"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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protein_id="AAS38632.1"
b_xref="GI:42733668"
b_xref="GI:42733668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNNSKSITATLRGOKRRSVOKGNPFSLLPLHERTFSFKGHWCFEIIDGEVNQIDVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.48;
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                                                                                                                                                                                                   TTTTTTAAAAAACCTAAATT
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ACCESSION
VERSION
KEYWORDS
SOURCE
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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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AUTHORS
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JOURNAL
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AC15379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H., Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M., Utterback,T.R., Sandiquel,P., Ma,J., Pontearoli,A.C., Rohlfing,T., Schubert,K., Sandiquel,P., Ma,J., Barbazuk,B., Bennetzen,J. and Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Char, A.P., Pertea, G., Zheng, L., Rabinowicz, P., Eraser, C.M., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Eraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Schubert, K., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a
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HTG; HTGS PHASE1.
Zea mays
Zea mays
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3 (bases 1 to 172293)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Utterback, T.R., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
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Seq_lib_id: ZOCF
------ Project informaton
Web_site: http://www.tigr.org/tdb/tgi/maize/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: maize@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 172293)
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5434: gap of unknown length
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/estimated 1 83497. 8359 /estimated 1 114545. 114 /estimated 1 116258 116 /estimated 1 19323. 119	yest_mated_length=unknown gap	## BOUICE 1. 1./233 // organism="Zea mays" // mol_type="genomic DNA" // strain="B73" // db xref="Faxon:4577" // clone="zwwBBb0131C15" 24222521 gap	** 66377 70549 70549 74168 74268 82176 82276 83497 114545 1114545 1114545 ** 1114545 ** 1114545 ** 1114545 ** 112369 ** 112369 ** 125460 ** 125460 ** 131581 131581 ** 131581 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 138688 ** 1386839 ** 156739 ** 167212 167212 168322
TITLE Direct Submission: JOURNAL Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850 REFERENCE 3 (bases 1 to 201985) AUTHORS Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and	-	Z C 706	/estimated_length=unknown 1215912148 gap

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FEATURES SOURCE Gap Gap Gap		TITLE JOURNAL COMMENT
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RESULT 14 AF034389/c LOCUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS SOURCE ORGANISM REFERRICE AUTHORS TITLE JOURNAL PUBMED	gap	gap gap gap
AF034389 - 713 bp DNA linear INV 04-FEB-1999 plasmodium falciparum sexual stage antigen (s16) gene, promoter and partial cds. AF034389 AF034389.1 GI:3098290 AF034389.1 GI:3098290 Plasmodium falciparum (malaria parasite P. falciparum) Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Eukaryota; Alveolata; Apicomplexa; Wirth,D.F., Eling,W., Konings,R.J., Kaan,A.M., Mbacham,W., Wirth,D.F., Eling,W., Konings,R.J., and Stunnenberg,H.G. Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite plasmodium falciparum Mol. Cell. Biol. 19 (2), 967-978 (1999) 9891033	Similarit Simila	/estimated_length=unknown 6521965318 /estimated_length=unknown 78775. ,78874 /estimated_length=unknown 8779887897 /estimated_length=unknown 9446494563 /estimated_length=unknown 121762121861 /estimated_length=unknown

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142
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Submitted (12-NOV-1997) Molecular Biology, University of Nijmegen, Submitted (12-NOV-1997) The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toernooiveld 1, Nijmegen 6525
Location/Qualifiers
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Dechering, K.J., Kaa
                                                                                                                                                                                                                                                                                                   CGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTTATATACATTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                    AATATTATCCTATGATAATAAAGCTATTGTGGAAATTATATTTTATGGAAAATATAATAT
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                                                                                            CTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTT
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711. .>713
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537. .>713
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537. .710
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.2; DB 2;
Pred. No. 0.0063;
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                                                          LBIYGELCETNPNPN"
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                                gene="migA"
                                               884. .2899
                                                                                                                                                                                                                                                                                                                                                                         product="MigA"
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Submitted (27-JAN-1997) Department of Biology, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on migA, a BTB protein
Mol. Biol. Cell 8 (9), 1763-1775 (1997)
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1 (bases 1 to 3576)

Escalante,R., Wessels,D., Soll,D.R. and Loomis,W.F.

Chemotaxis to CAMP and slug migration in Dictyostelium both depend
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                                                                                                                                                                                      951. .1289
/gene="migA"
/note="encodes |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="essential for slug migration" note="N-terminus of this protein is similar to other BTB domain proteins, such as the Mus musculus and human zinc finger proteins encoded by GenBank Accession Numbers U14556 and L16896, respectively"
                                                                                                                                       LYDIVELTPNAFWTKDVÞASWVMIDLGÞNRTVVÞMYYTIRHGLSYKSDSLRTWDFQGS
TNGEQWTVLKRHTNDÞSLNYKYATHSWÞVTGCETAFRYFRILQTGKNSNNRNFLVIGG
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gene="migA"
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gene="migA"
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chromosome="4"
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    Drosophila
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		432 ATTTTTTTATTTAATTTTATTTTTATTTTTTTTTTTT	Дb
		832 TTTGATTTTTCAAAAAAATTAGTTTATTTTCTCTTTAT 871	δ
	433	492 TTCAATCGCCTTTTGAATTTAGTTTTTTTTTTTTTTTTT	Db
	831	772 TCAAAAATÇITTCTGATTTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	Ş
	493	552 ACACAACACCACAATTGTTTTTTTTTTGTGTTTTTTTTTT	망
	771 .	712 TTTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGT	Ş
	553	612 TTGTTATTTTTGTTATTTTTAAATAATTTTATTTATACAATAAAATACTTTAAACACAAC	DЬ
	711	652 TATTTTGTTATTGTTTTTATATACATTTTCTCTCTTACAATAGAGTGATTTTCTTCCGA	Q
	613	672 AAAAAAAAAAAAAAATAATAGGGTGTGTGAAGAATTGTTTTTT	Вb
	651	592 AGCGACAAATTATATCGAAAGGTAAGGTATGACGTTCAGATTTTTTCTTTTTCATTCTTGT	ξ
	673	732 ТТТАЛЛАЛАТАЛЛАЛАТАЛЛАЛАТАЛАНТАЛАНАТАЛАЛТАЛАЛАЛТАЛТАЛТАЛАЛАЛ	Db
	591	532 CTTAAAAAACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAG	, vo
	733	792 ТАЛАЛАНТАЛАЛАТАЛАЛАТАЛАЛАЛАТАЛАЛАЛАТАЛАЛАСАЛАТТАЛАТТТТАЛ	8
	531	472 TAATCCACTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAAACCACGATCCT	Ş
	793	852 TATTTATTATTATTATTACTACAATTTTGTTTTTGTATAAAAAATTAAAAAATAAAAA	
	471	412 TGTCTAGTGTCCACTATTGGCACTACCCAGAACATATTAAAAAAATAACCAAAGTAAC	8.
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ALIGNMENTS

WPI; 1999-10 New nucleic	PA (PION-) PIONE XX PI Albertsen MC,	PR 23-JUN-1997;	PF 19-JUN-1998;	XX PD 30-DEC-1998	PN WO9859061-A1.	OS Zea mays.	KW Ms45; male KW plant tise		08-JUN-1999	AAX07408;	RESULT 1 AAX07408 ID AAX07408 s	
WPI, 1999-105628/09. New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.	(PION-) PIONEER HI-BRED INT INC. Albertsen MC, Fox TW, Garnaat CW, Huffman GA, Kendall TL;	97; 97US-00880499.	98; 98WO-US012895.	98	-A1.		Ms45; male; tissue-preferred; regulatory region; plant cells; plant tissue; differentiated; maize; hybrid seed; fertility; ss.	Zea mays Ms45 male tissue-preferred regulatory region.	99 (first entry)		T 1 408 AAX07408 standard; DNA; 1394 BP.	

The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile

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                                                The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding a M845 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production.
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Oy 1 CCATGGTGTCTTATTACTGAATGAGTGAAAAAAAAAAAA	that involves introperably linked to operably linked to all the fertility of the gene. A method of gene. A method of requence represents referred regulator and BP; 411 A; 31	A male tissue-preferred regulatory region comprising nucleotide sequency researchal for initiating transcription of the MS45 gene useful for presential for initiating transcription of the MS45 gene useful for promediating fertility in a male plant. XX PS Claim 4; Page 46; SOpp; English. XX CC The invention provides a male tissue-preferred regulatory region (I) CC CC comprising nucleotide sequences essential for initiating transcription CC CC the MS45 gene. A method of mediating male fertility in a plant is	PR 15-FEB-2000; 2000US-00504487. XX PA (PION-) PIONEER HI-BRED INT INC. XX PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL; XX XX XX XX XX XX XX XX XX	OS Zea mays. XX PN WO200160997-A2. XX PD 23-AUG-2001. XX PF 13-FEB-2001; 2001WO-US004527.	ID AAH76332 standard; DNA; 1394 BP. XX AAH76332; XX pr 29-OCT-2001 (first entry) XX	Oy 1081 TGAGATTGTGCGGTTTGGCAACGATAGCCACATAGCTCATAGCTCATAGGTGCCTACGTCA Db. 1081 TGAGATTGCGGTTTGGCAACGATAGCCACATAGGTGCCTACGTCA 1140 Db. 1141 GGTTCGGCAGCTCTCGTGTATCATAGCCACCATAGGTTGCCTACGTCA 1140 Oy 1141 GGTTCGGCAGCTCTCGTGTCACATGGCATACTACATCGTTGTTCAACCGTTCGTC 1200 Oy 1201 TTGTTCCATCGTCCAAGCCTTGCCTATCTCAACCAAGAGGATACCTACTCCAAACAAT 1260 Db. 1201 TTGTTCCATCGTCCAAGCCTTGCCTATCTCAAACCAAGAGGATACCTACTCCCAAACAAT 1260 Oy 1201 TTGTTCCATCGTCCAAGCCTTGCCTATCTCAAACCAAGAGGATACCTACTCCCAAACAAT 1260 Db. 1201 TTGTTCCATCGTCCAAGCCTTGCCTAACCAAGAGGATACCTACTCCCAAACAAT 1260 Oy 1261 CCATCTTACTCATGCAACTTCCATGCAAACAACCAAGAGGATACCTGTAAC 1311

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Best Local Similarity
Matches 1311; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an MS45 martissue preferred regulatory region from Z. mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
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    mays Ms45 male tissue-preferred regulatory region encoding

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CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAACTTCCACGGGTGCATGAT 120
                                                                                                                                                                                                                                                           CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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                                                                                                                                                                                                                              CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1311; DB 5; llarity 100.0%; Pred. No. 1.2e-269; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                            GGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGT 1204
                                                                                                                                                                                                                                                                                    12.3%; Score 160.6; DB 5, Imilarity 97.6%; Pred. No. 1.5e-24; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                 tion provides a male tissue-preferred regulatory region (I) nucleotide sequences essential for initiating transcription of gene. A method of mediating male fertility in a plant is hat involves introducing an expression vector comprising a perably linked to (I) into a plant where the exogenous gene ale fertility of the plant and (I) controls expression of the gene. A method of producing hybrid seeds is also provided. The squence represents a Z. mays Ms45 promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ssue-preferred regulatory region comprising nucleotide sequences for initiating transcription of the MS45 gene useful for fertility in a male plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           )0; 2000US-00504487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue; regulatory region; transcription; male fertility;
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55 BP; 59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
                                                                                             CCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 124
                                                                                                                         TCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 1264
                                                                                                                                                                                               cdcddarcccdrgrcarcrcacarddcaracracardcrrgrrcaaccdrrcgrcrrgr 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 8; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                          DB 5; Length 255;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.
plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2001
                                                                          Plant full length insert polynucleotide seqid 23340.
                                                                                                                21-APR-2005
                                                                                                                                                    ADX48600;
                                                                                                                                                                                       ADX48600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequence
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nes 157; Conserv
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                                                                                                                                                                                                                                                                                                                                                                              CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                         CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT
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                                                                                                                                                                                                                                                                                GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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nilarity 99.4%;
Conservative
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Pred. No. 1.7e-21;
D; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                            plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a recombinant DNA construct comprising a polynuclectide consisting of a sequence encoding an amino acid se available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynuc of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful in physical arrays of molecules of the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are also useful as a constant and the invention are als
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
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05-NOV-2001; 2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-180133/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .mproving yield.
                                                                                                                                                                                                                                                                                                Local
             911
                                                                  122
                                                                                                                                                                                                                      791
                                                                                                                                                                      62
                                                                                                                                                                                                                                                                        95;
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SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      content; gene; ss.
                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                                                        GCCCTAGAAT 920
                                                                  ATTAGTTTATTTTTCTTTGÁGAÁAÁTÁGÁÁTTĆCCTTGGGÁÁÁTTÁGÁGTTTCTÁAÁCGÁ
                                                                                                    ATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAATAGAGTTGCCAGACTA 910
                                                                                                                                                                      TTTTTAGGGCTAGTTTGGAAATCTCATTTTTTCAAGAGATTTTTATTTTCCTAAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         у <u>д</u>.
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                                                                                                                                                                                                                                                                                                                                                                       89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23340;
                                                                                                                                                                                                                                                                                                                                                                       A; 53
                                                                                                                                                                                                                                                                                             5.6%;
73.1%;
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                                                                                                                                                                                                                                                                     Score 74; DB
Pred. No. 4.6e
0; Mismatches
                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                       G; 112
                                                                                                                                                                                                                                                                        4.6e-06;
ches 35;
                                                                                                                                                                                                                                                                                                                                                                       T; 0 U;
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                                                                                                                                                                                                                                                                                                                          13;
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                                                                                                                                                                                                                                                                                                                     Length 320
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ADX33444

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ADX33444 standard;

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CC The invention describes a recombinant DNA construct comprising a copynucleotide consisting of a sequence encoding an amino acid sequence cavailable in electronic form from the US patent office at.

Cf. ftp.segdata.uspto.gov/sequence.html?DpcID:2004034888. The polynucleotide cof the invention are also useful in physical arrays of molecules and as compound plant tolerance to cold, heat, drought, herbicides, extreme common the conditions, pathogens or pests, for manipulating growth rate in compound to the call cycle pathway, for conferring compound to plant settle should be call cycle pathway, for conferring conference to plant disease, for producing galactomannam, complete to plant growth and development under at least one combination or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert conjuncted that can be used in the recombinant DNA construct of the convention.
Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tole: extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulate yield; plant growth; plant development; seed oil; protein yield; protein content; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant full length
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05-NOV-2001; 2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 16264; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-180133/17
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                                                                    Sequence
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KOVALIC D K.
SCREEN S E.
TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou Y,
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                     Similarity
5.6%;
milarity 73.1%;
Conservative (
                                                                      BP;
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                                                                      170
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                                                                    A; 119
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   Pred. No. 5.4e-06;
0; Mismatches 35
                     Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screen
                                                                    146 G; 189 T; 0 U; 0 Other;
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                                       DB 13;
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                                     Length 624;
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protein yield;
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RESULT 9
ADX61650
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      The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US pattent office at ftp.seqdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of
                                                                                                                                                                                                                           New recombinant DNA construct, useful for improving plant tol cold, heat, drought, herbicides, extreme osmotic conditions, pests, for conferring increased resistance to plant disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                galactomannan production;
yield; plant growth; plan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; herbicide tole extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance;
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05-NOV-2001;
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                                                                                                                                                                                      Claim 1; SEQ ID NO 32493; 15pp; English.
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                                                                                                                                                                                                                                                                                                                 Liu J,
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                                                                                                                                                                                                                mproving
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KOVALIC D K.

SCREEN S E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   content; gene;
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2001US-00985678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tion; lignin production; plant growth regulator; plant development; seed oil; protein yield;
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                                                                                                                                                                                                                                                             tolerance
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or for
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RESULT 10
ADX34996/G
ID ADX344996/G
ID ADX34496/G
AC ADX34
XX ADX34
XX ADX34
XX ADX34
XX ADX34
XX Plant
KW Plant
KW Plant
KW Plant
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Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; heatbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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                                                                             cold, heat,
pests, for o
                                                                                                                                                                                       WPI; 2004-180133/17
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                                                    improving yield
                                                                             recombinant DNA construct, useful for improving plant tolerance to d, heat, drought, herbicides, extreme osmotic conditions, pathogens ts, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1683
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                                                                                                                                                                                                                                                                                                                    ZHOU Y.
KOVALIC D K.
SCREEN S E.
TABASKA J E.
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                                                                                                                                                                                                                                                                                                 CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTAGTTCATTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTA 1742
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                                                                                                                                                                                                                                 , Y,
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2001US-00985678.
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73.6%;
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Pred. No. 1
                                                                                                                                                                                                                                            Screen
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ев 37;
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Claim 1; SEQ ID NO 17816; 15pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide CC of the invention are also useful in physical arrays of molecules and as CC plant breeding markers. The recombinant DNA construct is useful for CC plant breeding markers to cold, heat, drought, herbicides, extreme CC osmotic conditions, pathogens or pests, for manipulating growth rate in CC plant cells by modification of the cell cycle pathway, for conferring CC increased resistance to plant disease, for producing galactomannan, CC lignin or plant growth regulators, for increasing the rate of homologous CC content on in plants, for improving yield by modification of CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake CC or by providing improved plant growth and development under at least one cutes condition or for modifying seed oil or protein yield and/or CC content. This sequence represents a plant full length insert CC polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant protectant; plant growth regulant; gene therapy; plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; heat tolerance; drought tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield;
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(LIUJ/)
(ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                             06-MAY-1999;
05-NOV-2001;
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n content; gene; ss.
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                           ZHOU Y.
KOVALIC D
                                                                                    LIU J.
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Pred. No. 1.8e
0; Mismatches
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les 27;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes a recombinant DNA construct comprising polymucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at ttp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymof the invention are also useful in physical arrays of molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides; extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 31957; 15pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu J,
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(CAOY/)
                                                                              plant protectant; plant growth regulant; gene therapy, plant; recombinant DNA construct; physical array; plant breeding marker; cold tolerance; herbicide tolerance; cold tolerance; herbicide tolerance; extreme osmotic condition; pathogen tolerance; pest tolerance; growth rate; cell cycle pathway; disease resistance; galactomannan production; lignin production; plant growth regulator; yield; plant growth; plant development; seed oil; protein yield; yield; plant growth; plant development; seed oil; protein yield;
                                                                                                                                                                                                                                                               Plant full length insert polynucleotide segid 31061.
                                                                                                                                                                                                                                                                                                                                                                                                    ADX60218 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.8;
Pred. No. 2
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); Mismatches
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34888. The polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2537;
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1 sequence
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Unidentified.

07-DEC-2001

(first entry)

AAL15210

standard;

CDNA; 883

BP

2929

2989

AAL15210;

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RESULT 13
AAL15210/c
ID AAL152
XX
AC AAL152
XX
AC AAL152
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat drought, herbicides, extreme sometic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lighin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LIUJ/) LIU J.
(ZHOU') ZHOU Y.
(XOVA) KOVALIC D K.
(KOVA/) SCREEN S E.
(TABA/) TABASKA J E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polymucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens pests, for conferring increased resistance to plant disease, or for improving yield.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-1999; 99US-00304517.
05-NOV-2001; 2001US-00985678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2004034888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3607 BP; 915 A; 695 C; 718 G; 1279 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 31061; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-180133/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-2003; 2003US-00425114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CAOY/)
                                                                                                                                                                                                                                                 2930
                                                                                                                                                                               2990
                                                                                                                                                                                                                                                                                                                     2871 TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAA
                                                                                                                                                                                                              912
                                                                                                                                                                                                                                                                                    852
                                                                                                                                                                                                                                                                                                                                                        792 TITAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTTCAAAAAAA 851
                                                                                                                                                                                                                                                                                                                                                                                             105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAO Y.
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                      CCCTAGAATGTTTTCCCAATAAA 934
                                                                                                                                                                                                                                                                        TTAGTTTAGTTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG 911
                                                                                                                                                                                                                                                 CCCTTAATGTTTTTTTTCATGAA
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kovalic DK,
                                                                                                                                                                                                                                                                                                                                                                                                         5.5%;
                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Score 71.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screen
                                                                                                                                                                               3012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SE,
                                                                                                                                                                                                                                                                                                                                                                                             .4e-05;
es 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tabaska
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JE,
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3607;
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Human breast

cancer expressed

polynucleotide

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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human breast cancer expressed polynucleotides (AALD67544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1378; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide useful as a marker for the diagnosis of breast cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000;
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14-MAR-2000;
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                                                                                                                                                                                    599
                                                                                                                                                                                                                                                                                                                                                                          237;
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                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               883
                                                                                                                                                                                                                                                                                                                                                  TGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCA
AAAAAAATTTTTTNAAANTNTTTTTAAAACCTTNAATTNAAANANAATTTTTTTNNNTT
                        TCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATT
                                                                             ANATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAA
                                                                                                                          TTATTGTTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATA
                                                                                                                                                           AATAANTTNAATTTTTTTTAATNAAAAAAAAAATTTNAAATTTTAANCAANTNTTTTTT
                                                                                                                                                                              AATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTTCATTCTTGTTATTTTG
                                                                                                                                                                                                                TTAAANNTTTTNTAANTTATTAAACCAAAATTTTTTTTTAAAAAATTTTTTAAAANTT
                                                                                                                                                                                                                                       AACAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACA
                                                                                                                                                                                                                                                                   TANAAATTTTTTNAAAAACTAATTNTAANNATANTNAATTTTTNTAAAAAAANNNAAAAA
                                                                                                                                                                                                                                                                                            CTCGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAA
                                                                                                                                                                                                                                                                                                                        TGTTNANNNANACCTANACCTTTAAANATNTNNNANTTNAANNAAAAAAATATTTAAANN
                                                   Xu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0176077P.
; 2000US-0189167P.
2000US-0192099P.
; 2000US-0193480P.
; 2000US-0205230P.
; 2000US-0211315P.
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                                                                                                                                                                                      5.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                             A; 18 C;
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                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                         Score 70.2; DB 4;
Pred. No. 3.8e-05;
0; Mismatches 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             23 G; 396 T; 0 U; 124 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
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                        838
                                                   514
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                                                                                                                                                            634
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                                                                                                                                                                                                                                                                   754
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454
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Matches Query Match Best Local (

Similarity

5.4**%**; 39.2**%**;

0;

Score 70.2; DB 11; Pred. No. 3.9e-05; 0; Mismatches 367;

Indels Length

0

Gaps

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RESULT 14
ACN85231/c
ID ACN852
XX
ACN852
XX
AC ACN852
XX
AC CANCER
XX
DT 02-DEC
XX
CANCER
XX
US2003
XX
US2003
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IS-JUL
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IS-
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                                               The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cancer; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACN85231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACN85231
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated polypeptide associated with breast cancer, detecting presence of polypeptide in sample, as a marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2001; 2001US-0306220P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003099974-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breast cancer related marker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2002; 2002US-00198846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCT 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTNAAAAATAATTTTATANTTATNNAANANAAATTTAAAANTNAANANAAAAATTTTA
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   960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6381; 36pp; English
   B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour; cytostatic; marker; detection; therapy;
   340 A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĭ,
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flowering locus T gene; FT; terminal flower; TFL; Apetala3; Ap3; plant; floral development; plant sterility; plant fertility; flowering time; plant growth rate; inflorescence architecture; tissue culture morphology; cell division; FT homologue; gene; ds
Danilevskaya O, Hermon P, Bruggemann E, Shirbroun D, Rafalski JA, Sakai H, Cahoon E, Cahoon R, Klein T;
                                                                                                                                                30-JAN-2003; 2003US-00343477
                                                                                                                                                                                                    29-JAN-2004; 2004WO-US002422
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WPI; 2004-580996/56.

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New polynucleotides, specifically nucleic acid fragments encoding flowering locus T gene (FT) or terminal flower (TFL), or Apetala3 (Ap3) homologs, useful for floral development, e.g. engineering plant flowering time.

Claim 6; SEQ ID NO 63; 109pp; English

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The present invention describes an isolated polynucleotide comprising a complement encoding a polypeptide either having flowering locus T gene (FT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also (GFT), terminal flower (TFL), or Apetala3 (Ap3) homologue activity. Also (Gescribed: (1) a vector comprising the polynucleotide; (2) a recombinant DNA construct, (5) producing a plant comprising the cell with the polynucleotide; (4) a cell comprising the creombinant DNA construct; (5) producing a plant comprising transforming a cell with the polynucleotide, and regenerating a plant from the considerating; (6) a plant comprising transforming construct; (7) a seed comprising the recombinant DNA construct; (7) a seed comprising the recombinant DNA construct; (8) an construct; (7) a seed comprising at least 30 nucleotides, where the crist nucleotide sequence contains at least 30 nucleotides, and where the crist nucleotide sequence is comprised by another polynucleotide, where creative nucleotide sequence; (9) an isolated polypeptide having FT or Ap3 containing a cativity, as described above; and (10) isolating a polypeptide comprising the polynucleotide comprising isolating the polypucleotide comprising isolating the polypucleotide comprising the polypucleotide comprising the polypeptide from a containing a recombinant DNA construct comprising the polypucleotide coperably linked to a regulatory sequence. The polypucleotides are useful containing time, plant grown rate of cell division to enhance contained the rate of cell division to enhance contained to a sequence represents an FT homologue cransformation. The present sequence represents an FT homologue nucleotide sequence from the present invention.

Sequence 13400 BP; 3962 A; 2948 C; 2695 G; 3795 T; 0 U; 0 Other;

Matches Query Match Best Local 9 89; Similarity Conservative 73.6%; 0; Mismatches Score 69.8; DB 13; Pred. No. 9e-05; 32; Indels Length 13400; 0 Gaps 0,

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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ALIGNMENTS

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404 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCCAGAACAAGATTTAAAAAAAA	Query Match 69.3%; Score 908; DB 9; Length 963; Best Local Similarity 100.0%; Pred. No. 9.6e-180; Matches 908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/mul-y-projection / multiple / mu	Seq primer: TR Seq primer: TR Class: methylation filtered. Location/Qualifiers 1. 963 /organism="Zea mays" /mol type="qenomic DNA"	Contact: Catny Whitelaw TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Teax: 301-838-0208 Teax: 301-838-0208	whitelaw (C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw (C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Cohsortium for Maize Genomics Unpublished (2002) Unpublished (2002) Other SSS: OMDQ20TV	CC656933.1 GI:32060225 GSS. Zea mays Ze	CC656933 963 bp DNA linear GSS 19-JUN-2003 OGWDD20TM ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence.

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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 915)
Whitelaw.C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: GGIAGG8TH
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: "F
Class: methylation filtered.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                  TGACGITCAGAITTTTCTTTTTCATTCITGTTAITTTGTTATTGTTTTATATACATTTT
                                                                         GGAGAGAGAGAGAAATCAGTTTTAAGTCATTGTCCCTGAGATGTGCGGTTTGGCAA 1100
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                                                                                                                  AAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAG 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMEMa0715B15"
/clone=lib="ZM_0.7.1.5_KB"
/note="Vector: pBcSK-; Site_1: H/methylation filtered genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              51.8%;
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Pred. No. 9.5e-132;
0; Mismatches 0;
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1 (Dases 1 to 687)

1 (Dases 1 to 687)

Richiaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Unpublished (2002)
Unpublished (2002)
Contact: Cathy Whitelaw
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Location/Qualifiers
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Tel: 301-838-5943
Fax: 301-838-6208
Email: whitelnw@tigr.org
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                                                                                 AGTCATTGTCCCTGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAG
                                                                                                                                                                                 organism="Zea mays"
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/strain="B73"
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genomic survey sequence.
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Tel: 301-838-5843
Fax: 301-838-0208
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Class: methylation filtered
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Similarity 80.1%;
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Zea mays"
/mol type="genomic DNA"
/strain="B73"
/strain="B73"
/db xref="caxon:4577"
/clone="ZMMBMA0809B10"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Pred. No. 1.5e-09;
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AUTHORS
                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                           RESULT 6
CZ295176
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Best Local Similarity 78.6%;
Matches 110; Conservative
 TITLE
                                                                                                                 ORGANISM
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CL235046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bharti@waksman.rutgers.
Seq primer: SP6
Class: BAC ends
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Tel: 732 445 3801
Fax: 732 445 5735
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Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bro Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing, Sequencing of the maize genome at PGIR (2003c) Unpublished (2003)
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1 (bases 1 to 967)
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CZ295176
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                            1 (bases 1 to 860)
Bharti, A.K., Nelson, A.B.,
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ZMMBF0063M20f ZMMBF
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Construction,
               and Messing, J.
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Location/Qualifiers
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/clone="ZMMBBb0575001"
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/cultivar="B73"
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/clone_lib="ZMMBBb (HindIII)"
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Sequencing and
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Pred. No. 1e-08;
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                              Young, S.,
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                              Keizer,G.,
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ZMMBF0063M20
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ing, J.
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                              Zohovetz, V.,
 Fosmid Library
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Best Local :
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Tel: 732 445 3801
Fax: 732 445 5735
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Unpublished (2005)
Contact: Bharti, A.K.
                                                                                                       Maize Genomics Consortium Unpublished (2003)
Other GSSs: PUILO19TD Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
CG048704
CG048704.1 GI:33920884
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The Plant Genome Initiative at Rutgers, Waksman Institute,
                                            9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 814)

1 (bases 1 to 814)

1 (bases 1 to 814)

1 (bases 1 to 814)
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PUILO19TB ZM_0.6_1.0_KB
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Seq primer: TR
Class: sheared
                            Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                            Zea mays
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                                                                                                                                                                   Bennetzen, J
                                                                                                                                                                                    Resnick, A.,
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/cultivar="B73"
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/mol_type="genomic D
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/lab_host="EPI100-T1"
/clone_lib="ZMMBF"
/note="Vector: pEpiFOS-5;
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                                                                                                                                                                                   Fraser, C.M.,
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Indels Length 754;

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FEATURES
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AUTHORS
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CG414922/c
                                                FEATURES
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence. CG414922
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ZMMBBb0290L09.r ZMMBBb Zea mays genomic clone ZMMBBb0290L09 3',
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                                                                                                                                                                                                                               Sequencing of the maize genome Unpublished (2003)
Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A,
                                                               Plate: 0290 row: L
Seq primer: M13r
Class: BAC ends.
                                                                                                                                                                             Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                   and Wing, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTT 772
                                                                                                                 BACKWARD: M13r
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                                                                                                                                                  PRimers
                                                                                                                                                                                                                                                                                                                                                Kim, H.R., Hatfield, J., Soderlund, C.,
                                                                                                                                                                 rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="ZMMBTa0611C13"
/clone lib="ZM 0.6 1.0 KB"
/clone lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOFO; Site 1: EcoRI; 0.6-1.0 kb high
/note="Vector: PCR4-TOFO; Site 1: EcoRI; 0.6-1.0 kb high
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/strain="B73"
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                                Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 88; DB 10;
Pred. No. 7.1e-08;
0; Mismatches 90
                                                                                                    column:
                                                                                                    9
                                                                                                                                                                                                                                    P.O. Box 210088, Tucson,
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                                                                                                                                                                                                                                                                                                                                                      Bharti, A.K., Messing, J
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Matches 126
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Zea mays
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genomic survey sequence.
CC439901
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUHRV15TD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases I to 950)

whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Can Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC439901
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                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                               Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                              Similarity
             ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGATTTTTTATTTTTTCAAT 183
                                  ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTCAAA 846
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                                                                                                                                                                                                                                                                                                                                                              whitelaw@tigr.org
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
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db_xref="taxon:4577"
                                                                                                                                                           /clone="ZMMBTa519D06"
/clone lib="ZM,0.61.0 KB"
/clone lib="ZM,0.61.0 KB"
/clone="Vector: pCR4-TOPO; Site_1:
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                             organism="Zea mays"
mol_type="genomic DNA"
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                                                                              Score 86.8; DB 9; Length 950; Pred. No. 1.3e-07; O; Mismatches 47; Indels
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EcoRI; 0.6-1.0 kb high

Gaps

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RESULT 11
CC400575/c
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CC384247
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                                                                                                                                                                                                                                             714 TTATAAAATGACTATAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTC 773
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CC384247
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1 (bases 1 to 652)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC384247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bennetzen, J.
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                                                                                                         TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAA
                                                                                                                                                               AGAATCTTATTTATTAATGTTAAGAGCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301-838-5843
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                                                                                                                                                                                                                                                                                                                                      /clone="ZMMBTa495L13"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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Pred. No. 1.4e-07;
0; Mismatches 74;
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Y., San Miguel,P., Ma,J. and
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ZMMBTa495L13,
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CC400574
CC400574.1 GI:
GSS.
Zea mays
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                                                                                      CC400574 BZM_0.6_1.0_KB Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
Other_GSSs: PUHLU61TB
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Resnick, A., Fraser, C.M., Yuan, Y.,
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Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 797)
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Seq primer: TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                   TTGATTTTTTCAAAA-AAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAA 891
                                                                                                                                                                                                                                                                                                                                                                                         TAAAGGACAAGAAACATTTTTTAAGAGCTAGTTTGGTAATCCCATTTTTTTCAAAGGATT
                                                                                                                                                                                                                        AATTATTTGGCCAGCCCCATAAATTATTTAAAC 984
                                                                                                                                                                                                                                                                                          AAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTAT
                                                                                                                                                                                                                                                                                                                        TTCATTCTCACAAGGGAAAAATAGTTTATTTCCCCTTTTGTAAAATGGTAATCACTCGGAA
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                                                                                                                                                                                             ATTTCAAATTCCACTTTGCAAAATAGTGTCATC 305
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/clone="ZMM_0.6_1.0 KB"
/clone="Vector: pCR4_TOPO; Site_1:
/note="Vector pcR4_TOPO; Site_1:
CoT selected genomic DNA library"
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/mol_type="genomic DNA"
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                                                 GI:30880664
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Pred. No. 1.4e-07;
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Y., San Miguel,P., Ma,J. and
                                                                                             DNA linear GSS 19-MAY-2003 genomic clone ZMMBTa480L01,
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a; Poales; Poaceae; PACCAD
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RESULT 13
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Zea mays
Zea mays
Entaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Entaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 471)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                             CG103452 471 bp DNA linear GSS 20-AUG-2003 PUJBE19TB ZM 0.6 1.0 KB Zea mays genomic clone ZM/BTa0628D13, genomic survey sequence.
CG103452
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1 (Dases 1 to 820)

Whitelaw; C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
Other_GSSs: PUHLU61TD
                                                                                                                                                                                                                        CG103452.1 GI:33985746
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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Pred. No. 1.4e-07;
D; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
Zea mays
                                                                                                                                                                                                                                                            Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFQX12TB
Contact: Cathy Whitelaw
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CG082135 CG082135.1 GI:33964429
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Other GSSs: PUJBE19TD
Contact: Cathy Whitelaw
                                                                                                                      Class: sheared ends.
                                                                                                                                                          9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Spermatophyta; Magnoliophyta; Liliopsida; Poalea; Poaceae; PACCAD
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/clone=lib="ZM 0.6_1.0_KB"
/clone="Wector: pCR4-TOPO; Site 1: EcoRI;
/coT selected genomic DNA library"
  /db_xref="taxon:4577"
                     organism="Zea mays"

ol_type="genomic DNA"

strain="B73"
                                                                                               ocation/Qualifiers
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(mol_type="genomic DNA")

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Pred. No. 2.4e-07
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                                                              665
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1 (bases 1 to 781)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Padiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Other_GSSs: OGUCG53TH
Contact: Cathy Whitelaw
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CoT selected genomic DNA library"
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Oy 907 ACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAAATTATTTG 960
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546 ACTAGCCCTAAAGTATTTTATAAAATAGAGGAAAAATTCGTCTATTTTCATTG 493

Search completed: March 6, 2006, 01:57:48
Job time: 6189.32 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: PATCHION DATA: CONCURRENT APPLICATION DATE: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                  TELEPHONE: (515) 248-4
TELEPAX: (515) 248-484
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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STREET: Box 1000
CITY: Johnston
STATE: Iowa
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ZIP: 50131
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LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
US-08-880-499-2
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FOX, TIM W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Rendall, Timmy L.
ITIE OF INVENTION: MALE TISSUE-PREFERED REGULATORY REGION
TITLE OF INVENTION: MALE TISSUE-PREFERED REGULATORY REGION
TITLE OF INVENTION: MALE TISSUE-PREFERED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: BOX 1000
CITY: Johnston
STATE: Dox 1000
CITY: Johnston
STATE: Low 2000
CITY: Johnston
STATE: Low 1000
CITY: 
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US-08-880-499-2
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                                                                                                         Query Match
Best Local Similarity
Matches 1311; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
  CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC
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Fox, Tim W.
                                                                                                            100.0%;
llarity 100.0%;
Conservative 0;
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                                                                                                               Score 1311; DB 3;
Pred. No. 8.7e-305;
, Mismatches 0;
                                                                                                                                                                    Length
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Db 5606 TCTACG		.200	GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 12	_
. Qy 792 TTTAAG		1140		μ.
Query Match Best Local Similar Matches 93; Con		1080 1140		
; IMMEDIATE SOURC ; LIBRARY: mai ; LIBRARY: (gt ; CLONE: pMgfil US-08-968-542C-1		1020 1020 1080		
ANTI-SENSE: no criginal source creamism: ma TISSUE TYPE:	<u></u>	60	TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG 960 	2-1
TOPOLOGY: 1ii MOLECULE TYPE: DESCRIPTION: HYPOTHETICAL: 1	<u></u>	8 %	TTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGT 900 	
SEQUENCE CHARACT LENGTH: 6027 TYPE: nuclei	·· ·	. 40 . 0	TTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTC	
TELECOMMUNICATION TELEPHONE: (71: TELEPHONE: (71: TELEPAX: (71:		80 80	ATGACTATAAAGTCATTTTTATATAAAGAGCÁGGCATGTCGTAGATTCTCGTTCAAAAATC 780 	7-7
; ATTORNEY/AGENT : ; NAME: Benjam: ; REGISTRATION L	•	720 720	ATTGTTTTATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAA 72	4-4
CLASSIFICATION PRIOR APPLICATION APPLICATION NU FILING DATE:		60 .	TRIATCGAAAGGTAAGCTATGACGTICAGATTTITCTITTTCATICTTGTTATITTGTT 660	H—H
SOFTWARE: Mic CURRENT APPLICAT APPLICATION NO FILING DATE:		00	CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAACATCTAAGAGCGACAAA 600 	0-0
3999		40	CGAAAGCTATCATGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540 	0-0
22		80 0	TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480	н
		20 0	GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420	ae
g g g g		6 6	TTATTATTCTTTAGATATTATTTAÀTTTTTGGAAAAATAACAAACTTATACTTTTGTGTA 360 	н—н
RESULT 3 US-08-968-542C-1/c ; Sequence 1, Applica ; Patent No. 5981728	<u> </u>	8 8	CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300	0-0
Db 1261 CCATCTI		.5 5	CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	ი—ი
1201			CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTGCTAT 180	0-0
Db 1141 GGTTCGG	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	120 120-	CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	α—a

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DABLE FORM:

28: 3.5 floppy disk

Apple Macintosh
SYSTEM: Macintosh
Microsoft Word 6.0.1 for Macintosh
JCATION DATA:

28: No. 591728ember 12, 1997

XTION DATA:

N NUMBER:
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eic acid
45: double-stranded
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|amin Aaron Adler, Ph.D., in the property of t
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SEQ ID NO: 1:
ACTERISTICS:
                                                                                                                                                           5.1%; Score 66.4; DB 2; Length 602 arity 77.5%; Pred. No. 5.2e-06; Dnservative 0; Mismatches 26; Indels
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erg, et al.
TION: dull1 Codes For A No. 5981728el Starch
TION: Synthase
ENCES: 35
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|10; pMg6Aa; pMgt6-2M
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McGregor & Adler, LLP
1 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA to mRNA
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                                                                                                                                                                                                                                                    Length 6027;
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GENERAL INFORMATION:
APPLICANT: Myers, Martha G.
APPLICANT: Myers, Martha G.
APPLICANT: James, Martha G.
TITLE OF INVENTION: dull1 Coding for a No. 66
TITLE OF INVENTION: dull1 Coding for a No. 66
TITLE OF INVENTION: Thereof
FILE REFERENCE: D0036PCT
CURRENT APPLICATION NUMBER: US/09/554,467A
CURRENT FILLING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: PCT/US98/24225
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 08/062,102
PRIOR FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 37
SEQ ID NO 1
LENGTH: 6027
TYPE: DNA
ORGANISM: maize
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US-09-554-467A-1/c
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US-08-410-784A-3/c
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; OTHER INFORMATION: CDNA sequence corresponding to the gene encoding the
; OTHER INFORMATION: starch synthase enzyme DU1.
US-09-554-467A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09554467A Patent No. 6639125
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Patent No. 5912413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: MYERS, ALAN M.
APPLICANT: JAMES, MARTHA G.
                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,784A
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ISOLATION OF SU1, A TITLE OF INVENTION: ENZYME, THE PRODUCT TITLE OF INVENTION: SUGARY 1
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin and Hayes LLP
STREET: Ten Post Office Square
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                       STREET: Ten P
CITY: Boston
STATE: MA
                 FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                 ZIP: 02109
                                                                                                                                                                                                                                       COUNTRY:
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Similarity 77.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08410784A
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                                                                                                                                                                                                                                   USA
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                    24-MAR-1995
)N: 800
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OF THE
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MAIZE GENE
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                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.

APPLICANT: Peterson, David S.

APPLICANT: Su, Xin-Zhaun

APPLICANT: Wellems, Thomas E.

APPLICANT: Wellems, Thomas E.

APPLICANT: Wellems, MINDING DOM

TITLE OF INVENTION: BINDING DOM

TITLE OF INVENTION: AND PLASMOD

NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATIN:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Heine, Ph.D., Holliday C
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: ISU-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-2290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: GO HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2523 base pair
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nuclear STRANDEDNESS:
                                                                                                                                                                                                                                                                      STREET: 620 Newport
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617-451-0313
                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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NAME: Israelsen, Nec
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             894 ATAGAGTTGCCAGACTAGCCCTAGAAT 920
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                                                                                                                                                                                                                                      92660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACATATACATATACATATAATAAGGTCTAGTTTGACAATCCTATTTTATCAAAAG--TTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACATTTTTTCAAATAAATTAGTTTATTTTCTCTTGA-AAAATAGGAATTTCTCAGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2523 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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0 Newport Center Drive
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                                                                                                                                                                                                                                                                                                                                                                                          BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                               US/08/487,826B
  29,655
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Pred. No. 0.00029;
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                                                                                                                                       Version
                                                                                                                                                                                                                                                                                                               Bear
16th Floor
                                                                                                                                       #1.25
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US-08-487-826B-13
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                                                                                                                                                                        US-09-662-254B-26
                                                                                                             Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 69331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.3%;
Best Local Similarity 50.2%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bawden, Alison Louise
TITLE OF INVENTION: Materials and Methods for Delivery and Expression of Heterologou
TITLE OF INVENTION: Vertebrate Cells
FILE REFERENCE: UF-221C1XC1
                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 50000
                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/224,479
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/662,254B CURRENT FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Moyer, 1
APPLICANT: Li, Yi
APPLICANT: Bawden
                                                                                                                                                                                         ORGANISM: Amsacta moorei entomopoxvirus
                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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LENGTH: 19124 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: NITELECOMMUNICATION INFORMATION: TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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FILING DATE: 1998-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15437 GTTTTTATATTTCTTTTTTAATATAAATACATATATAAA 15397
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                     854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     614 TAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTTTTATAT 673
                                                      315 ATATTATTTAATTTTTGGAAAAATAACAAACTTATACTTTTGTGTAGGGCCTCAGCATAG 374
                                                                                                               Similarity
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAATT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAATTTTTTTTTAATTTTTTTTTTGATAATCTTTTTCATTTTTTATTCTATCAAAAATTTA 15558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09662254B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richard W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235-0176
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                                                                                                             45.1%;
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                                                                                                                                                                                                                                                                                                                                                             09/086,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 2; Length 19124; Pred. No. 0.0014; 0; Mismatches 140; Indels
                                                                                             0,
                                                                                                             Score 56.4; DB 3; Pred. No. 0.0026;
                                                                                             Mismatches
                                                                                             306;
                                                                                                                                Length 50000;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                             Gaps
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                                                                                                                                                                                                         NAME/KBY: misc_feature; OTHER INFORMATION: Incyte ID No. 6476212 700350078H1; NAME/KBY: unsure; LOCATION: 10, 12, 185-186, 204, 253, 274, 278; OTHER INFORMATION: a, t, c, g, or other US-09-313-294A-5397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-313-294A-5397
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                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PER
SEQ ID NO 5397
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Lalgud
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27432 AAAAGAATATTTATAATACATTATACATA 27403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27732 ATTAAAAGAAGAAAATAATTAATTACAAAGATTTAATATGAATATGAAAAATTTTATAAA 27673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27792 ТАЛАТАТАСАЛАТАТТАЛТАЛТАЛТАСАЛТАЛТАЛТСТТАЛАЛАТАЛАСАЛТТАТТАЛА 27733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608 GAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTTGTTATTGTTT 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 TAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 TACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 ATTITCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTGTCCACTATTGGCAC 434
849 AAATTAGTTTATTTTCTCTTTAT-AAAATAGAAAACACTTAGAAAAAATAGAGTTGCCAGA
                                                                                             789 TTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAAAA 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           728 TAAAGTCATTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGA 787
                                                             w
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                                                             TTCCTAANGNCCTAGTTTGGAAACCCCATTTTCCCCACGGGTTTTTCATTTTCCCAAGGG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAATTAGTTTATTTTCTCTTTTATAAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TICGATAAATTATTTAAAGTAGGCAAGACTGATAATTTATCTTCTAGACAATCAAATTT 27553
                                                                                                                                                                                                                                                                                                                                                                                                                        PERL Program
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raghunath V.
                                                                                                                                                    4.3%;
                                                                                                                                   Score 55.8; DB 3;
Pred. No. 0.00065;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           877
                                                                                                                                       39;
                                                                                                                                                                            Length 279;
                                                                                                                                       Indels
                                                                                                                                       1;
                                                                                                                                         Gaps .
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RESULT 9
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-880-499-1/c
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, NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(1.5849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1357
LENGTH: 612
THE TRANSPORT OF SEC OF THE TRANSPORT OF THE TRANSPO
                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08880499
Patent No. 6037523
GEMERAL INFORMATION:
APPLICANT: Albertson, Marc C.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Myxococcus xanthus
                        APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127;
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nilarity 51.4%;
Conservative
PIONEER HI-BRED INTERNATIONAL, INC
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RESULT 11
US-08-880-499-2/c
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                                                                                                                                                                                              APPLICANT: Albertson, Marc C.
APPLICANT: Albertson, Marc C.
APPLICANT: Fox, Tim W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
APPLICANT: Kendall, Mare Tresqui
                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08880499 Patent No. 6037523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.2%;
Best Local Similarity 55.8%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
APPLICATION NUMBER: US/08/880,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy
                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER H
                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O. STREET: Box 1000 CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1394 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800
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COUNTRY: U
                                      CITY: Johnston STATE: Iowa
                                                                        STREET: Darwin Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            761 TAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTTAGTTTGGCAACCCTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               881 AACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTTTTCCCCAATAAATTACAA 940
                                                                                                                                                                                                                                                                                                                                                                                                                                      770 CGAGAATCTA 761
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: Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACACAGTGATTGTAATTTATTTGGGAAAACATTCTAGGGCTAGTCTGGCAACTCTATTTT 891
                   Iowa
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACTGTGTA 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCAAAGAATTTTGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAAAAATTAGAA
                                                                                         Darwin Building,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                 Timmy L.

MALE TISSUE-PREFERRED REGULATORY REGION
AND METHOD OF USING SAME
                                                                                           HI-BRED INTERNATIONAL, INC. lding, 7100 N.W. 62nd Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 0.0012;
0; Mismatches 84;
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N. C. Caldelle

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RESULT 12
US-09-806-708B-23
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                                                                          ; OTHER INFORMATION: US-09-806-708B-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.2%;
Best Local Similarity 55.8%;
Matches 106; Conservative
                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 1055
  Query Match 4.2%; Score 55.4; DB 3; Length 1055; Best Local Similarity 22.5%; Pred. No. 0.0013; Indels 15. Matches 182; Conservative 181; Mismatches 430; Indels 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Applicate Patent No. 6784342 GENERAL INFORMATION:
Best Local Similarity 22.5%; Pi
Matches 182; Conservative 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1394 base naturally type.
                                                                                                                                                                                                                                                                                                                                  APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/147,133 PRIOR FILING DATE: 1999-08-04
                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                NAME/KEY: promoter LOCATION: (1)..(10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     761 TAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTC 820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGAATCTA 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACTGTGTA 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCAATAAATTACAA 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCAAAGAATTTTGATTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09806708B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1394 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                              consensus sequence of A.t. and L.a. FAE1 promoters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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  Indels 15;.
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-004-056-1/c
                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Calgene LLC
                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09004056F Patent No. 6566586
SEQ ID
                                                                        TITLE OF INVENTION: Plant Expansin Promoter Sequences FILE REPERENCE: 125
CURRENT APPLICATION NUMBER: US/09/004,056A
CURRENT FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 60034914
EARLIER FILING DATE: 1997-07-01
                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1057 AMATCAGITITAAGICATIGICCCIGAG 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 СТААТССАСТСБАААБСТАТСАТБТААТБТ---ТТАААБАААСАТСТАТТААААССАСБА 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 WYGASWAGNASTRRTTYTWRWKWMCKRKSARARATRGRARYMRAWYTAWARRTGWTKAMA 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITTGTGTAGGGCCTCAG-CATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCC 410
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SEQ ID NO 53
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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                                                                                                                                        US-09-640-173-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 53, Application US/09640173
Patent No. 6613515
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Best Local (
                                                                                  Query Match
Best Local Similarity
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                                                                      Matches
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APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: OVERIAN TUMOR SEQUENCES
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 210121.484C2
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/640,173
CURRENT FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 196
SOPTWARE: FastSEQ for Windows Version 3.0
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LOCATION: (956)
OTHER INFORMATION: unknown nucleotide
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LOCATION: (947)
OTHER INFORMATION: unknown nucleotide
                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C
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LOCATION: (930)
OTHER INFORMATION: unknown nucleotide
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                       TTTTTCTTTTTCATTCTTGTTATTTGTTATTGTTTTTATATACATTTTCTTCTCTTACA 691
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Pred. No. 0.0019;
0; Mismatches 128;
                                                                  Score 55; DB 3; Length 396
Pred. No. 0.0011;
0; Mismatches 178; Indels
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GENERAL INFORMATION:
APPLICANT: XL, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF OV
FILE REFERENCE: 210121.484C4
CURRENT APPLICATION UMMBER: US/9/713,550
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 205
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 396
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US-09-713-550-53
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Patent No. 6617109
                                                                                                                                                                                                                                                                                                                                Query Match 4.2%;
Best Local Similarity 43.8%;
Matches 139; Conservative
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NAME/KEY: misc_feature
LOCATION: (1)...(396)
OTHER INFORMATION: n = A,T,C or
-09-713-550-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                  CGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAA 811
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      AAATTACAATCACTGTG
                                                                                              ÄÄTTCÄNÄÄÄÄAGAANÄAGÄÄÄÄÄNÄTÄANANNNÄNCNNÄNNNNNNNATNNTNCTTNATA 310
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                                                                AAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAATGTTTTCCCCAAT 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09713550
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                                                                                                                                                                                                                                                                                                                                               Score 55; DB 3;
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                   Mismatches 178;
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                                                                                                                                                                                                                                                                                                                                                             Length 396;
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Search completed: March 5, 2006, 22:36:25 Job time : 367.534 secs THIS PAGE BLANK (USPTO)

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Title:
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                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
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Gapop 10.0 , Gapext 1.0
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1311
1 ccatggtgtctctatcaaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq3:*
                                                                                                                                                                                                                                                              NEW PUB.seq:*
NEW PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query Match Length DB

ij

Description

119036

GUELY MACCH. Best Local Similarity 57.3%; Pred. No. 0.0063; Best Local Similarity 57.3%; Pred. No. 0.0063; Matches 142; Conservative 0; Mismatches 105; Indels Matches 142; Conservative 105; I	, D	Seguence 182, App	716-11-091-883-182
JULY MALCH. Best Local Similarity 57.3%; Pred. No. 0.0063; Best Local Similarity 57.3%; Pred. No. 0.0063; Matches 142; Conservative 0; Mismatches 105; Indels 670 ATATACATTTTCTTCTCTTACAATAGAGTGATTTTCTTCCGATTTTA 670 ATATACATTTTAGATTCAGTCAGCAAAAGCTAACATTATGTTTGCTTCTTC 391 ACATAGTTTTAGATTCAGTCAGCAAAAGCTAACATTCTCGTTCAAA 730 AAGTCATTTTTATATAGAGCACGCATGTCGTAGATTCTCGTTCAAA		sequence 29/105/	US-09-925-065A-29/109
JULY MALLY STAR Pred. No. 0.0063; Bet Local Similarity 57.3%; Pred. No. 0.0063; Matches 142; Conservative 0; Mismatches 105; Indels 670 ATATACATTITCTTCTCTTACATACAATACAGTGATTTTCTTCCGATTTTA 670 ATATACTTTACATTCTGCAAAAAGCTAACATTATGTTTGCTTC 391 ACATACTTTACATTCTGCTCAGCAAAAAGCTAACATTCTCGTTCCAAA	Ş	Sequence 13297, A	US-09-925-065A-13297
JULY MALCH SIMILARITY 57.3%; Pred. NO. 0.0063; Best Local Similarity 57.3%; Pred. NO. 0.0063; Matches 142; Conservative 0; Mismatches 105; Indels Matches 142; Conservative 0;	?	Sequence 667265,	US-09-925-065A-667265
Watch watch to call Similarity 57.3%; Fred. No. 0.0063; Best Local Similarity 57.3%; Fred. No. 0.0063; Indels Watches 142; Conservative 0; Wismatches 105; Indels 670 ATATACATTTCTTCTTACAATACAGTGATTTTTTTTTTCTTCCGATTTTTA	מט	Sequence 667263,	US-09-925-065A-667263
Justy match Similarity 57.3%; Pred. No. 0.0063; Best Local Similarity 57.3%; Pred. No. 0.0063; Best Local Similarity 0; Mismatches 10; Indels Matches 142; Conservative 0; Mismatches 170; Indels Matches 142; Conservative 0; Mismatches 170; Indels	!	Sequence 667262,	US-09-925-065A-667262
Jury Macuity 57.3%; pred. No. 0.0063; Best Local Similarity 57.3%; pred. No. 0.0063; Indels Matches 142; Conservative 0; Mismatches 105; Indels Matches 142; Conservative 0; Mismatches TUTTCYCATTUTTA	ş	Sequence 26, Appl	US-10-330-773-26
Similarity 57.3%; Pred. No. 0.0063; 2; Conservative 0; Mismatches 10	•	Sequence 25, Appl	US-11-121-086-25
Similarity 57.3%; Pred. No. 0.0063;	Mac	Sequence 242, App	US-10-330-773-242
Cimilarity E7 3%; pred No 0 0063;	. Bes	Sequence 11, App1	US-10-240-708-11
	Que	Sequence 803045,	US-09-925-065A-803045
	•	Sequence 13314, A	US-10-995-561-13314
US-II-014-0/I-2	US-11-	Sequence 63, Appl	US-10-240-708-63
CIRER INFORMATION: FOO		Sequence 73, Appl	US-10-240-708-73
CONTINUE TAILOUR DOE		Sequence 803046,	US-09-925-065A-803046
TOTATION (1) (1002)		Sequence 54272, A	US-09-925-065A-54272
TEMALORE:		Sequence 534, App	US-10-330-773-534
CASSACTOR . Dea may		Sequence 36, Appr	US-10-240-708-36
OBCANICM. 700 mays	 2 5	Sequence 2, Appli	US-11-014-071-2
LENGTH: 1092	 !E		

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	46.2	46.2	46.2	46.2	46.4	46.6	46.6	46.8	46.8	47	47.2	47.2	47.4	47.6	48	48	48.2	48.2	48.2	48.6	49	49	49.8	49.8	49.8	•
	3.5	3.5	3. 5	3.5	3.5	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.6	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.7	3.8	3.8	3.8	
	6499	6499	3219	3219	6499	86899	9347	8961	8537	19233	10619	6070	173602	6113	108057	6499	355211	8467	5152	583	10467	583	4339	677	677	
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	sequence st, Appr	Sequence //, Appr	``	sequence /14059,	Sequence 90, Appr		Sequence 35, Appr	, a	4 0		٠,٠	, 5	Sequence 25, Appr	sequence 13, Appl	Sequence 835, App	•	Sequence 242, App	-	~	1001		ع د				

ALIGNMENTS

음 성	B 8	Query M Best Lo Matches	PEA NAM LOC OTH	SEQ ID NO LENGTH: TYPE: DI ORGANISI	PRIOR	CURRENT CURRENT PRIOR A	APPLIO APPLIO APPLIO TITLE TITLE	ESULT 1 S-11-01 Sequer Public GENER! APPLI
730 AAGTCATTTTTATATAAGAGCACGCATGICGTAGATTCTCGTTCAAAAATCTTTCTGATT 789	670 ATATACATTTTCTTCCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATA 729	Query Match 5.2%; Score 68; DB 11; Length 1092; Best Local Similarity 57.3%; Pred. No. 0.0063; Matches 142; Conservative 0; Mismatches 105; Indels 1; Gaps	PEATURE: NAME/KEY: promoter LOCATION: (1)(1092) OTHER INFORMATION: P95 11-014-071-2	Q ID NO 2 LENGTH: 1092 TYPE: DNA ORGANISM: Zea mays	PRIOR FILING DATE: 2004-07-29 NUMBER OF SEQ ID NOS: 2 SOFTWARE: FastSEQ for Windows Version 4.0	CURRENT APPLICATION NUMBER: US/11/014,071 CURRENT FILING DATE: 2004-12-16 PRIOR APPLICATION NUMBER: 60/530,478 PRIOR APPLICATION NUMBER: 60/530,478 PRIOR PILING DATE: 2003-12-16 DETOR APPLICATION NUMBER: 60/591,975	APPLICANT: Hershey, Howard F. APPLICANT: Unger, Erica APPLICANT: Wu, Yongzhong TITLE OF INVENTION: Dominant Gene Suppression Transgenes and TITLE OF INVENTION: Methods of Using Same TITLE REFERENCE: 1554	-2 Application US/11 No. US20050246796 ORMATION: Cigan, Andrew M. Fox, Timothy W.
510	õ	1.						

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US-10-240-708-36
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CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
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SEQ ID NO 36
TENGTH: 9347
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Best Local Similarity
Matches 155; Conserv
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Publication No. US20050282157A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: OLEK, Alexander
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                          910
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                                    AAAAATTAGTTTATTTT 863
                                                                                                                                                      TAATATTTTTTGTTGTTTTTATGAATGTAATGTTTTTTTCGTATTGTTTTTTGTTTTGTT
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                                                                                                                                                                                                                                                                  TTTATATACATTTTCTTCTTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACT
                                                                          ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTCAAA
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  8846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57.8; DB Pred. No. 0.64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                162; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9347;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-773-534
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US-10-330-773-534
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT EILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
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Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
                                                                                                                                                                                                                                                                                                                                              Sequence 54272, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 981
SOFTWARE: FRANSEQ for Windows Version 4.0
SEQ ID NO 534
LENGTH: 254396
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Best Local Similarity
                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201611 TTTGTCATAATTGTÄÄTCÄTTTTAGGCTTTTTTÄÄÄÄÄ 201648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAATCAAATGGCATTAGAATTTAGAACAACTTCTAAATCATCGTGAGGTATTTTTCCTAT 201610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCATGTCGTAGATTCTCGAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTGGCAA 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAACTGGGGTTTTTTTTTTCAGCAACTTAAATAAAGAAAAGTCAGCTTTACTACAGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTGTTTCTTCAAAGAATTTTGATTTTTCAAAAAA 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>ATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCA</u>
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Pred. No. 3.
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; ORGANISM: Homo sapiens
US-09-925-065A-54272
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PRILING DATE: 2000-10-24
PRIOR PRILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-01-06
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FREESEQ FOR WINDOWS VETSION 4.0
SEQ ID NO 803046
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US-09-925-065A-803046
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54272
LENGTH: 915
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Best Local Similarity 51.0%;
Matches 151; Conservative
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                                                                                                                                                  Matches 137; Conservative
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPPLICANT: Wang, David G.
RITLE OF INVENTION: Identification and Mapping of Single
RITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 ACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATT 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            715 TATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 TTGTTATTGTTTTTATATACATTTTCT-TCTCTTACAATAGAGTGATTTTCTTCCGATTT 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 ATATACATTTCTTCTCTTACAATAGAGTGATTTCTTCCGATTTTATAAAATGACTATA 729
                                                                                                610 AAGGTAAGCTATGACGTTCAGATTTTTCTTTTTTCATTCTTGTTATTTTTGTTTATTTTTT 669
                                                                   37
                                                            ATGACATGGTCAGACTTTCTGATTTGTTCTGAACATCCTTTTCTTTTAAACAACCAGTTA 96
                                                                                                                                                                     4.1%; Score 53.6; DB 6; Length 488; 49.3%; Pred. No. 1.7;
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Pred. No. 1.2;
1; Mismatches 143; Indels
                                                                                                                                                       ed. No. 1.7;
Mismatches 140; Indels
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724 ACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTT 783	3897 TATTTTTAAAATTTTAACTTATTTTAAATTCAAAAAATATATATACAAATTTATTA	665 TTTTTATATACATTTT-CTTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATG:723	3957 TATAACTATTATTATATTAAAAAAATACTTTAAAATTTTTT	605 ATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTGTTATTTGTTATTG 664	545 CATATTTCCAAAGACAAATATGTTACACTTTACAAACATCAACAACAACAACAACAACAACA		CACGATCCTCTTAAAAAACAAG	4137 CTACAATCCCAACTACTCAAAAATCTCAAACAAAAAATAACTTAAACCCAAAAATTCAA 4078	425 CTATTOGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAA 484	y Match 4.1%; Score 53.6; DB 8; Length 5152; Local Similarity 48.2%; Pred. No. 3; hes 219; Conservative 0; Mismatches 224; Indels 11; Gaps 2;	YAHUKE INFORMATION: chemically treated genomic DNA (Homo sapiens))-240-708-73	ORGANISM: Artificial Sequence	•်ဗီဋ	APPLICATION NUMBER: D	APPLICATION NUMBER FILING DATE: 2000-	APPLICATION NUMBER: D	APPLICATION N	APPLICATION NUMBER: PCT/ APPLICATION NUMBER: PCT/	ENT APPLICA	E OF INVENTION: I		73, Appli ion No. US INFORMATIO	708-73/c	277 TGTTCTTTTTTTTTTTTTTTTAGAAAAAAAAAAACACTT 314	850 ARTTAGTTTATTTTCTCTTTATAAAATAGAAAACACTT 887	217 CTGGTTCCTTTTACTTTGTTTTATATATAACTTTAAATAAGCTTTGAATTAGACAAAACA 276	790 TTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTTGATTTTTTTCAAAAA 849	157 TABACTCTTTTTTACCTCAAAAACTACCTCTTTACAACTTTCTTTACATTTTTT	730 AAGTCATTTTTATAAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATT 789	97 TTTTATTTTAGGACTAAACTTACTACACAGGATTCTTTCT

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APPLICANT: DIERENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERNIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013,1012
CURRENT EPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/BP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 63
SEQ ID NO 63
SEQ ID NO 63
SEQ ID NO 65
PRIOR SEC ID NOS: 98
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                    RESULT 8

US-10-995-561-13314/c

; Sequence 13314, Application US/10995561

; Publication No. US20050272054A1
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US-10-240-708-63
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Best Local S
Matches 140
GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) -10-240-708-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity tes 140; Conserv
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                                                                                                                                                                                          TAGTTTATTTTCTCTTTATAAAATAGA 879
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                                                                                                                                                                                                                                       Application US/10240708
No. US20050282157A1
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ilarity 52.4%;
Conservative
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Pred. No. 3.3;
0; Mismatches 126;
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                                              CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
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US-09-925-065A-803045
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13314
LENGTH: 119036
                                                                                                                                                                                                                                                                                                   Sequence 803045, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: GENETIC POLINGOPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT EPPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                 PRIOR
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               FILING DATE: 2001-01-16
APPLICATION NUMBER: US 60/289,846
FILING DATE:
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Pred. No. 7.4;
0; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 119036;
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                                                                                                                                                                 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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SOFTWARE: FRATSEQ for Windows Version
SEQ ID NO 803045
LENGTH: 488
                                                                                         Query Match
Best Local S
Matches 218
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BERLIN, Kurt
APPLICANT: BERLIN, Kurt
TITIE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITIE OF INVENTION: by Assessing DNA Methylation
FILE REPERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03971
                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/EPO1/0397:
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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PPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                       ID NO 11
                                                                                                                                                                                                                                                        ENGTH: 6317
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DE 10032529.7
                   424 ACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGA
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al Similarity 48.9%;
136; Conservative
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                                                                                           Conservative
                                                                                                        3.9%;
45.8%;
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Pred. No. 7.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 242
LENGTH: 355211
                                                                                                                                                                                                                                                                                                                                    Matches 211;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
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APPLICANT: Marc Malandro

ITLE OF INVENTION: Novel Compositions and Methods in Cancer

ILE REFERENCE: 529452001300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(355211)
                                     61734 TATTTTATATATTTTATATATATATGTATATTTTATATATATATATATATATATATATATATATA
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                                                                                                                                               563 AATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATG 622
                                                                                                                                                                                                                     503 AAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACA
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683 TCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAAGTCATTTTTAT 742
                                                                       840 TTTCAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAAT 895
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Similarity 46.1%;
11; Conservative
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Pred. No. 1
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US-11-121-086-25
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
FILE REFERENCE: 09138.6000-00000
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.9%;
Best Local Similarity 45.5%;
Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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                                                                                                                                                                                   TTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTC
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TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAA
                                                                                                     TTÄTÄTÄÄTATGTTTÄTATATTATTATATTTÄTATAATATGTTTATATATTATTATATTTT 136837
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US-10-330-773-26
; Sequence 26, Application US/10330773
; Publication No. US20060040262A1
; GENERAL IMPORMATION:
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US-10-330-773-26
                                                                                                                  RESULT 14
US-09-925-065A-667262
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Best Local :
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1)...(68741
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llarity 46.2%;
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Sequence 667262, Application US/09925065A

Publication No. US20040181048A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hume
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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APPLICANT: Marc Malandro
TITLE OF INVENTION: NOvel Compositions and Methods in
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: US 60/243,096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCG
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RESULT 15
US-09-925-065A-667263
Sequence 667263, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
USANG. David G
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Best Local :
                                      APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-108-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
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-09-925-065A-667262
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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APPLICATION NUMBER: US 60/252,147
FILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
FILING DATE: 2000-11-30
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NG DATE: 2000-11-30
ICATION NUMBER: US 60/261,766
NG DATE: 2001-01-16
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US-09-925-065A-667263
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Best Local Similarity 45.6%;
Matches 214; Conservative
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 667263
LENGTH: 677
TYPE: DNA
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Pred. No. 5.4;
1; Mismatches 251; Indels
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Search completed: March 6, 2006, 10:32:49
Job time: 1371.54 secs

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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-425-115-14826
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Sequence 3, Appl.
Sequence 134230, Sequence 13420, As Teguence 16264, A Tuence 141826, Parce 32493, As Teguence 16264, As Tuence 34493, As Teguence 16264, As Tuence 34493, As Teguence 17816, As
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	25-13	25-13	5-11	25-13	73-12	25-11	25-11	5-11	5-11	5-11	0-35	5-11	9-04	4-26	5-11	5-11	5-11	5-11	5-11	5-11	5-11	5-11	
	5-48	5-2	5-3	5-15	26-38	5-16	4-83	4-77	5-17	420	2-10	5-41	8-11	2-1	4-20	4-16	5-14	4-30	5-14	4-17	5-49	5-75	
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241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCCACAATCGTCACCTATA 300	181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240 181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	121 CTCCATGTTCCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	121 CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT 180	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	1 CCATGGTGTCTCTATGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGTCC 60	/ Match Local S hes 1311		SEQ ID NO 1 LENGTH: 1394	NUMBER OF SEQ 1D NOS: 24 SOFTWARE: PatentIn Ver. 2.0	PRIOR FILING DATE: 1997-06-23	CURRENT FILING DATE: 2003-11-14	3	TITLE OF INVENTION: USING SAME	MALE T	HUPFMAN,		APPLICANT: ALBERISEN, WAKE C. APPLICANT: FOX, TIMOTHY W.	ORMATION:	Publication No. US20040221331A1	US-10-713-381-1

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                CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
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APPLICANT: ALBERTSEN, MARC C.:
APPLICANT: ALBERTSEN, MARC C.:
APPLICANT: GARNAAT, CARY
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHER TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: 08/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea may8
US-10-713-381-2
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Best Local Similarity 100.0%;
Matches 1311; Conservative 0
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Pred. No. 6.2e-275;
; Mismatches 0;
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; ORGANISM: Zea mays
US-10-713-381-9
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Publication No. US20040221331A1
GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                     SEQ ID NO 9
                                                                                                                                                                                                                      APPLICANT: FOX, TIMOTRY W.
APPLICANT: FOX, TIMOTRY W.
APPLICANT: GARNAN, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMOY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: US/10/713,381
PRIOR APPLICATION FILE 2003-11-14
PRIOR APPLICATION DATE: 1997-06-23
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    Score 160.6; DB 8;
Pred. No. 7.6e-25;
0; Mismatches 4;
                                          Length 255;
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENOTH: 1261
TYPER: NEW ACID NOS: 369326
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION UNMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 158
TYPE: DNA
ORGANIEM: Zea mays
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US-10-425-115-134230

; Sequence 134230, Application US/10425115

; Dublication No. US20040214272A1

; GENERAL INFORMATION:
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US-10-713-381-3
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Best Local Similarity
Matches 157; Conserv
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAN, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMOTY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
TYPE: DNA
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No. US20040221331A1
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                                                                                                                                                                                        and Other
                                                                                                                                                                                        Molecules
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APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cop invention: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 23340
LENGTH: 320
TYPE: DNA
ORGANISM: Zea mays
US-10-425-114-16264
Sequence 16264, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
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US-10-425-114-23340
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Publication No. US20040034888A1
GENERAL INFORMATION:
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Local Similarity 78.2%;
nes 97; Conservative
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                                                                                                                                                                                                                                                                                              ATTAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTA 910
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ilarity 73.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 74; DB;
; Pred. No. 6e-0:
0; Mismatches
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Pred. No. 3.9e-07;
0; Mismatches 27;
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RESULT 8
US-10-425-115-141826
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                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 141826
LENGTH: 1326
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Best Local
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                                                                                                                                                                                                 Matches 114;
                                                                                                                                                                                                                                     Query Match
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APPLICANT:
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: MRT4577_60829C.1
                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Clone ID: LIB3062-023-G10_FLI
                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                  816 GITTCTTTCAAAGAATTTTGATTTTTCAAAAAAAATTAGTTTATTTTCTCTTTATAAAA 875
                                                                                                                                                            756 TGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCT 815
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         TAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCCTAGAAT 920
                                                                                                                        TGAAGTTGGTGGTTGTGCTGGTATTTCACCTTTAACTGTAAGGACTAATTTGGGAACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao,
                                                                                                                                                                                                 Conservative
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73.1%;
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Pred. No. 8.3e-06;
0; Mismatches 35;
                                                                                                                                                                                                                     Score 73; DB 8; Length 1326; Pred. No. 2e-05;
                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                   50;
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                                                                           OTHER INFORMATION: Clone ID: MRT4577_175978C.1 US-10-425-115-83293
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Best Local S
Matches 106
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Publication No. US20040034888A1
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 83293
LENGTH: 2729
                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21 (53222)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-425-115-83293/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
Best Local Similarity 60.
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays FEATURE:
                                                                                                                                        PEATURE:

NAME/KEY: unsure

LOCATION: (1)..(2729)

OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 32493
ENGTH: 2445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pence 83293, Application US/10425115
Scation No. US20040214272A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1683 ATTAGTTCATTTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTA 1742
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                                                                                                                                                                                                                                                DNA
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Similarity 73.6%;
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Screen, Steven E
Tabaska, Jack E
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                     5.6%;
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Pred. No. 2.9e-05;
0; Mismatches 37;
; Score 72.8; D:
; Pred. No. 3.1e
0; Mismatches
                         DB 8;
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                                          Length 2729;
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US-10-425-115-51470/c
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US-10-425-114-17816/C
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Best Local Similarity
                                                                                                                                      Sequence 17816, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITIE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITIE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 369326
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(1203)
OTHER INFORMATION: unsure at all n locations
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LENGTH: 1203
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                                                                                                                                                                                                                                                                                                                                                                                   1130 GAAAATTAGTTTATTTTCTCTTGGAAAAATAAAAATCCCCGTAGAAAAATAGAGTTTCCAA 1071
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                                                                                                                                                                                                                                                                                                   1070 ACTAGCTCTAAGAT 1057
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                                                                                                                                                                                                                                                                                                                                         907 ACTAGCCCTAGAAT 920
                                                                                                                                                                                                                                                                                                                                                                                                                           847 АЛАДАТТАСТТТАТТТСТСТТТАТАЛАДТАСАДАДАДАСАСТТАСДАДАДАДТАСАСТТСССАС 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1203
INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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                                     Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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76.1%;
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APPLICANT: La ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Oth
TITLE OF INVENTION: Nucleic Acid Molecules and Oth
FILTE REFERENCE: 38-21(5.3222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 142853
LENGTH: 1123
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
RESULT 14
US-10-425-114-31957
, Sequence 31957, Application US/10425114
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US-10-425-115-142853/c
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17816
LENGTH: 928
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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Publication No. US20040214272A1
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·10-425-115-142853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     804 TTTTTAAGAGCTGGTTTGGCAA-CCTCATTTTTCTAAGGATTTCTATTTTACTAAGAAA
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                                                                                             702
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Similarity 78.0%;
99; Conservative
                                                                                                                             AGCCCTA 916
                                                                                                                                                               AATTAGTTAATTTTCT
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                                                                                                                                                                                                                                TITTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAA 849
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78.0%;
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                                                                                                                                                                                                                                                                                                 Score 71.8; DB 8;
Pred. No. 3.3e-05;
0; Mismatches 27;
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APPLICANT: KOVALIC, DAVID K.

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
ITITLE OF INVENTION: Nucleic Acid Molecules and Other TITLE OF INVENTION: Plants and Uses Thereof for F
FILE REFERENCE: 38-21(5313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31957
LENGTH: 2537
                                                                                                                                                                                                                                                                                                                         APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 52216
SEQ ID NO 52216
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US-10-425-115-52216
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; OTHER INFORMATION: Clone ID: MRT4577_147620C.1
US-10-425-115-52216
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                                                                                                                                                        Matches
                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                      105;
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                      TTAGTTTATTTTCTCTTTATAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAG 911
                                                                            TCTTAGGGCTAGTTTGAGAACCCT-TTTTTCCCAAAAGATTTTCATTTTTCAAAGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCTTAATGTTTTTTTTCATGAA 1940
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                                                                                                                TTAGTTCATTTTTCCTTGAGAAAATAGGAATCCCTTAAAAAAATAGTGTTTTCAAACTAG
                                                                                                                                                      Conservative
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Pred. No. 4.9e-05;
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SUMMARIES

Result

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ALIGNMENTS

Qy J	Db Qy	QQ V	Query Match Best Local : Matches 15	source ORIGIN	FEATURES	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	RESULT 1 AX224402 LOCUS DEFINITION ACCESSION VERSION
121 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157 	61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 120	1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	Match 100.0%; Score 157; DB 6; Length 255; Local Similarity 100.0%; Pred. No. 5.6e-40; es 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1. 255 /organism="Zea mays" /mol_type="unassigned DNA" /db_xref="taxon:4577"	PIONEER I-REED INTERNATIONAL, INC. (US) Location/Qualifiers	Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. and Kendall,T.L. Male tissue-preferred regulatory region and method of using same parent. WO 0150007-1 9 23-ANG-2001:	Zea mays Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	AX224402 255 bp DNA linear PAT 10-SEP-2001 Sequence 9 from Patent WO0160997. AX224402 AX224402 GI:15554644 AX224402 GI:15554644

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PD 30-OCT-2001
PD 30-OCT-2001
PF 19-UN-1998 JP 199504910
PR 23-UN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W PI TIMMY L KENDALL
PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C07K14/34, C1201/68, PC A01H5/00
CC Strandedness: Single;
PC A01H5/00
CC Strandedness: Single;
PC Topology: Linear;
PC Topology: Linear;
PC Topology: Linear;
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Homo sapiens
Male tissue-preferred regulatory region and method of using Patent: JP 2001520523-A 2 30-CCT-2001; PIONEER HI BRED INTERNATIONAL INC PN JP 2001520523-A/2
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Mammalia; Eutheria;
                                                                     Hominidae; Homo.

1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W.,

Kendall, T.L.
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BD062177.1 GI:22607782
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                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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23-JUN-1997 US 08/880499
MARC C ALBERGYSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUF
TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PF 19-UN-1998 JP 1999504910

PR 23-UN-1997 US 08/880499

PI WARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFWA

PI TIMMY L KENDALL

PC C12N15/82, C12N15/29, C12N9/24, C12N9/22, C12N9/10, C12N9/00 PC

C07K14/34, C12Q1/68,

PC A01H5/00

CC Strandedness: Single;

CC Topology: Linear;

CC Topology: Linear;
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Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoideae; Andropogoneae; Zea.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                 /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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Patent W00160997.
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Pred. No. 5.6e-40;
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a; Poales; Poaceae; PACCAD
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Hi-Bred Intl. Inc., 7300 N.W.
IA 50131-1004, USA
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/db_xref="taxon:4577"
  /organism="Zea mays"
/mol type="genomic DNA"
/culfivar="B73"
/db xref="taxon:4577"
/chromosome="91"
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Pred. No. 5.6e-40;
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Sequence 3 from Patent W00160997.
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AX224396 I GI:15554638
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Zea mays; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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RIMRYMLEGPRAGEVEVFANLPGFPDNVRSNGRGQFMVALIOCKTPAQEVFAKRPWLR
TLYFKFPLSLKVLTWKAARRWHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK
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TGELYVADAYYGLMVVGQSGGVASSVAREADGDFIRFANDLDVHRNGSVFFTDTSWRY
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dyrpvkhelapygevmgswprdnasrlrrgrlefvgevegpesiepdlograpyagna
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gene="Ms45"
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protein_id="AAK52489.1"
db_xref="GI:14028757"
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oin(1392. .1768,1898. .2182,2280.
gene="M845"
                                                                                                                                                                                                                                                  /organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577".
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Pred. No. 2.1e-36;
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Pred. No. 5.5e-40;
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124 CTTCCATGCA 133
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Pred. No. 1.8e-06;
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                                                                                                                                                                                                                                                                                                                  regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32974 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded single subclone. Region 18678-18873 is a double stranded single subclone. Areas 69957-70761, 89836-90416, 98951-9909, 105316-105607, and 133052-133152 are covered by Monsanto only. The nucleotide sequence of this BAC clone was generated by combining syngents, Monsanto and Arizona Genomics Institute sequencing data.
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Wing,R.A., Yu,Y., Soderlun
Collura,K. and Thompson,S.
Direct Submission
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Submitted (16-APR-2003) Clemson University Genomics Institute,
Submitted (19-APR-2003) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
On Jan 11, 2003 this sequence version replaced gi:24635991
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arizona, 303 Forbes, Tucson, AZ 85721, USA
5 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H., Rambo,T.,
Saski,C., Henry,D., Thompson,S., Simmons,J., Thurmond,S.K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-JAN-2003) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-NOV-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arizona, 303 Forbes, Tucson, AZ 85721, USA
3 (bases 1 to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Saski,C.,
Currie,J., Collura,K. and Thompson,S.
Direct Submission
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Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R.,
Currie,J., Collura,K. and Thompson,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryza.
1 (bases I to 137327)
Wing,R.A., Yu,Y., Soderlund,C., Kim,H.-R., Rambo,T., Currie,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC135206 DNA linear Oryza sativa (japonica cultivar-group) chromosome 3 OJ1041F02, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC135206.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ubmitted (09-OCT-2002) Arizona Génomics Institute, University of rizona, 303 Forbes, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:27596977
                                                                                                                                                           lone="0J1041F02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soderlund, C., Kim, H.-R., Rambo, T., Currie, J.,
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                                                                                                                                                                                                                                               (japonica cultivar-group)"
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Query Match Best Local S Matches 60

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SAPDIDKKIRALKKKIRLAEAQVQGDPENLKPEQLEKMKKIEGMKEELKLLENKSSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLETQGIMDYSLLLGVHFRNDYSVSKIGISQHIAFPKSTGKRKSFEGGSSFCELCFVE
SGCKDRDLIDSRKPFIQLGINMPAQAERSSKKILDNFLLNERHLFITPPSGGSCDVYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGSKFTPPHHSVDFRWKDYCPAVFRHLRKLFGVDPAEYMLAICGNDTLRELASPGKSG
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KIHRRFDLKGSSHGRTIDKTERKIDETTTLKDLDLQYAFRLQRFWYEELMKQIQMDCT
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19263. .19454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16734. .16878
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                                                                                                                                                            codon_start=1
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CTTCCATGCA 133

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CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 123

CCTTGGCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACGCTGACTCATGCAA 119440

Matches Query Match Best Local :

Local

Similarity

34.4%;

Conservative

0,

Score 54; DB 15; Pred. No. 1.8e-06; 0; Mismatches 10;

10;

<u>,</u>

Gaps

0

Length 137327; Indels

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MITE-adh, type G-like"

note="putative MITE,

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.62196)

Castaway-like"

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119439 CCTCCATGCA 119430

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RLERYLLPVYPPKLSQSIRGPAFVDYLLSSMSQISQLERMSLSCKASSKQRRCRQPRH
REGENELES
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AX224399
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AUTHORS
TITLE
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ORGANISM
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Zea mays
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HTG
                         Zebrafish DNA sequence
BX950854
                                                                                                                                                                                                                                                                                              Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. Male tissue-preferred regulatory region and method Patent: WO 0160997-A 6 23-AUG-2001, PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sparmatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade; Panicoideae, Andropogoneae; Zea.
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Sequence 6 from Patent WO0160997.
AX224399
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Sequence
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          BX950854.12 GI:58190604
                                                   BX950854
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Male Lissue-preferred regulatory region and
Patent: WO 0160997-A 5 23-AUG-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AX224399.1 GI:15554641
                                                                                                                                                                              Similarity
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                                                                                                                                                               25.5%; So ilarity 100.0%; I Conservative '0;
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5 from Patent WO0160997.
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/db_xref="taxon:4577"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e.; phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

The FOLLOWING SUBCOPT; Tr. TREMBL; WP:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the this is found the longest good quality representation will be submisted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery system (Zhirong Bao and Sean Eddy, submitted), a beginning (dar' were identified by Rick Waterman (Stephen lab, WashU). For further information see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-125M22 is from a CHORI-211 BAC library
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'fish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 25, 2005 this sequence version replaced gi:56368832.
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Contact: zfish-help@sanger.ac.uk
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Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 171896)
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ACACGCACATATGTTTCCTGAA 156
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/db_xref="taxon:7955"
/clone="CH211-125M22"
/clone_lib="CHORI-211"
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Submitted (04-DEC-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens BAC clone RP11-525L16
AC104134
                 The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from
                                                                                                                                                           Mapping information for this clone was provided by Dr. Wes Warre Department of Genetics, Washington University, St. Louis Mc. For additional information about the map position of this sequence, http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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University School of Medicine,
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Submitted (20-MAR-2002)
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Submitted (15-FEB-2002) Genome
University School of Medicine,
MO 63108, USA
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Doebber, A., Haakenson, W. and Tomlinson, C.
The sequence of Homo sapiens BAC clone RP11-525L16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: submissions@watson.wustl.edu
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GIVIKVSVADWKVMAFSKKGGHLEWEYGFCTPIASAWLLKDGKVIPISLFDTTSYTSN
DDVLEDEEDIVEAARGATENSVYLGMYRGQLLVLQSSVRISEKFPSSPKALESVTNENA
IIPLFTIKWKPLIHSPSERTPVLVGSDBFDKCLSNDKFSHEEYSNGALSILQFFYDNGY
YLPYYKRERNKRSTQITVRFLDNPHYNKNIRKKDPVLLLHWWKEIVATILFCIIATTF
IVRRLFHPHPHPHRQRKESETOCOTENKYDSVSGEANDSKWNDIKNGYISRYLTDFEFFI
IVRRLFHPHPHPHRQRKESETOCOTENKYDSVSGEANDSKWNDIKNGYISRYLTDFEFFI
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93417. .93529,95828. .96048,97969. .98091,98748. .98888,
100430. .100592,100805. .101039,103259. .103392,
105456. .>105650)
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100430. .100592,100805. .101039,103259. .103392,
105456. .105650))
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                                                                                                                                                                                                                                                                                                             note="Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA.; H_NH0525L16.2 This gene was based on gi(21361154) continued from H_NH0450E09.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (join (67723.
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TSTCHFTYPASHDLHLAQGDPNQVLQSADFPCLYDDKHOPAAEMAKGYLLLPGCPCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Homo sapiens hypothetical protein
(FLJ25369), mRNA.; H_NH0525L16.1
This gene was based on gi(22749356)"
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/clone_lib="RPCI-11"
4046. _4309
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/product="unknown"
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Query Match Local Similarity 87633 87693 87753 ACCTCCAAG 87761 123 Kamat, A., Karatas, A., Kalis, C., MacConald, P., Major, J., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Meneus, L., Micol, R., Norbu, C., Mergar, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Sponcer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. 63 Direct Submission
Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 214946) Took, A., vous., Ferreira, P., FitzGeralu, ..., Crand-Pierre, N., Hales, ..., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hales, ..., Johnson, R., Jones, C., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hagos, B., Karatas, A., Kells, C., Landers, T., Levine, R., warien, R., Karatas, A., Kells, C., Macdonald, P., Major, J., Marien, C., Macdonald, P., Major, J., Mihova, T., 3 TGTCATCTCACATGCCATACTACATGCTTGTTCAACCGTTCGTCTTTGTTTCCATCGTCCAA 62 Boguslavkiy, L., bum-Birren, B., Nusbaum, 70; Barna, N., Bastien, V., Bloom, Camarata, J., Chang, J., Chaza Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Homo sapiens (human) 214946 bp DNA li Homo sapiens chromosome 15, clone RP11-86001, AC136896 Birren,B., Nusbaum, AC136896.6 GI:29135656 xren,B., Nusbaum,C. and Lander,E. lomo sapiens chromosome 15, clone RP11-86001 upublished lominidae; Homo. (bases 1 to 214946) rren, B., Nusbaum, ACTICCATG 131 TCCTCCCCTATTCTTACCCTTTGTTCCATCTACTCCAGAACTCTCACCATTCTCCATACC 87752 GCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCA 122 TGGGATTACAAGCGTGAGCCACTGTACCTGGCCAACCTATCTTTTTCTTCCTCTCTTCCA 87692 (bases 1 to 214946) Conservative Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Kiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chee, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Far, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B. IGNHCANKLTAPKPTSSKSSEATLSISPPRPTTLSLDLTKNTTEKLQPSSPKVYLYI*...
QMQLCRKENLKOWMORCTIEERERS VCLHIFLQIAEAVEFLHSKGLMHENDLKESNIF
FTMDDVVKVGDPGLVTAMODEREGYTLTEMPAYARHTGOVGTKLYMSPEQIHGNSYS
HKVDIFSLGLILFELLYPFSTQMERVRTLTDVRNILKFEPLFTQKYPCEYYMVQDMLSP
SPMERPEAINLIENAVFEDLDFPGKTVLRQRSRSLSSGTKHSRQSNNSHSPLPSN" '* APSPQRSRSFSVG1SCDQTSSSESQFSPLEFSGMDHEDISESVDAAYNIQDSCLTDCD VEDGTMDGNDEGHSFELCPSEASPYVRSRERTSSSIVFEDSGCDNASSKEEPKTNRLH 22.0%; Score 34.6; DB Pred. No. 3.6; OB Mismatches 0; Bloom, T., Boguslavkiy, L., Boukhgalter, Chazaro, B., Choepel, Y., Collymore, A., urellano, K., Dewar, K., Diaz, J.S., Dodge FitzGerald, M., Gage, D., Galagan, J., Lander, E., Ali,A., DB 8; 59; Allen, N., Anderson, S., iy, L., Boukhgalter, B., Length 110127; Indels near PRI 21-MAR-2003 complete sequence. Gardyna, S., 0; Choepel, Y., Dodge, S., Gaps

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Matches

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4 (Dases I to 214946).

Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Chelloguelavkiy,L., Boukbgalter,B., Camarata,J., Chang,J., Checlano,K., Cook,A., Cooke,P., Corum,B., DeArellano,K., Collymore,A., Cook,A., Cooke,P., Corum,B., Erickson,J., Fi
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Nguyen, C., Nicol, R.,
O'Neil, D., Oliver, J
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Mar 21, 2003 this sequence version replaced gi:27877278
repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
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/clone_1b="RPC1-11 Hum
/clone_1b="RPC1-11 Hum
complement(1...362)
/rpt_family="HAL1"
complement(823...1431)
/rpt_family="L1MC5"
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complement(2941. .3295)
                                          complement(3307. .3311)
/note="<30 qual SNGL region"
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mol_type="genomic DNA"
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i., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
ioung,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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/rpt_family="GA-rich"
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/rpt_family="MLT1A1"
/rpt_family=14008. .4166
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/rpt family="L3"
5935. .6412
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complement(13183..13354)
/rpt_family="MIR"
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/rpt family="L1M1"
complement(19375. .20142)
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/rpt_family="MIR"
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/rpt_family="L3"
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10252
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/rpt_family="MIR"
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                       /rpt_fa
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/rpt_family="MLT2B3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35805 ATCCAACATACTAAGAAAAGAAGGTAGCTTTCTTAACCCAATAAATGTAACCTATGAAAA 35864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 TCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCGTCTATCGTCCAAGC
                                                                                                                                                                               Assembly program: XGRP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 141058 bases at least Q40
Consensus quality: 14124 bases at least Q30
Consensus quality: 141289 bases at least Q20
Insert size: 141354; sum-of-contigs
Insert size: 151351; 10.9% error; agarose-fp
Quality coverage: 8.68x in Q20 bases; sum-of-contigs
Quality coverage: 8.12x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-JAN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiriles: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 15, 2005 this sequence version replaced gi:56309949.
                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 141554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR847532.4 GI.57863691
HTG; HTGS PHASE1; HTGS ACTIVEFIN; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ріесев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR847532 141554 | Danio rerio clone DKEYP-86C9,
                                                                                                                                                                                                                                                                                                                                                                                            Center project name: zKp86C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATCTCTATGGGCAGAAAAATCATTTGACAAAATTACGCATTCTTCCATGATGTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="MLT1D" 36941. .37015
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Pred. No. 4.2;
0; Mismatches
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Search completed: March 5, 2006, 21:55:45 Job time: 687.29 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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                                                                        90222 ACAGTGACCCCTACATCCTTGTGCCTCAATGCATATTGTACAAGTGTACAGAGGTTTGGGT 90281
                                                                                                                                                                                    72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                        12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTCCATCGTCCAAGCCTTGGCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-86C9"
/clone_lib="DanioKeypilot"
/clone_1ib="DanioKeypilot"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:00290"
42428. .141554
/note="assembly_fragment:00621.0"
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10479...42327
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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Gapop 10.0 , Gapext 1.0
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Match Length
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10014.946 Million cell updates/sec
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Copyright (c) 1993 - 2006 Biocceleration
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Adb72455 Mouse Nfa
Ade95965 Mouse Nfa
Adp67076 Human mit
Aaa51436 A. thalia
Adb08983 Alloiococ
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AAX07408 Zea mays
AAX07409 Zea mays M
AAN76332 Z. mays M
AAN76332 Z. mays M
AAN76334 Z. mays M
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	28.4	28.6	28.6,	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.6	28.8	29.2	29.2	29.4	29.6	29.8	30	30	30	30.2	
	18.1	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.2	18.3	18.6	18.6	18.7	18.9	19.0	19.1	19.1	19.1	19.2	•
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	AAF15843	ADB92108		ADB87934	ADB20845	ACF62730	ABD32806_5	ACN45162	ADX13304	ADX11599	ABN67847	ADW26566	ADD71973	AAS32893	AAS32892	ADS57339	ADA68284	AAT42063_06	AAL62902	AAF22303_2	ADF00796	AAH13328	ADD33404	ADD33403	AAH76335	ADB12064_07	
	Aaf15843 Human pro	Adb92108 Human MUK		Human	- 3	Act62730, Cancer Da	Continuation (6 or		Adx13304 Plant rul	Adx11599 Plant Iul	trepto	Adw26566 Glycine m	Add71973 Human uri	Aas32893 Human gen	Aas32892 Human gen	Ads57339 Bacterial	Ada68284 Arabidops	Continuation (/ or	Aal62902 Vernonia	Continuation (3 or	ACTOUTY6 Bacterial	Aanisse Human CDN	Add33404 Mouse mit	Add33403 Mouse mit	Aah76335 Z. mays M	Continuation (8 or	;

ALIGNMENTS

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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The	Example 5; Fig 8; 50pp; English.	A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.	WPI; 2001-514772/56.	Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;	(PION-) PIONEER HI-BRED INT INC.	15-FEB-2000; 2000US-00504487.	13-FEB-2001; 2001WO-US004527.	23-AUG-2001.	WO200160997-A2.	Zea mays.		male tiegue. remulatory	Z. mays Ms45 promoter fragment.	29-OCT-2001 (first entry)	AAH76340;	RESULT 1 AAH76340 AAH76340 standard; DNA; 255 BP.

represents a Z. mays Ms45 promoter fragment

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                                                                                                                                                                                            Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0
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157; Conserv
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Pred. No. 2.4e-42;
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Pred. No. 1.4e-42;
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maize; hybrid seed;
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                                                                         AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                                                                                                                                                                                                                               100.0%; Score 157; DB 2; llarity 100.0%; Pred. No. 2.4e-42; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     232
                                                                                                                                                                                                                                                                                                                                                                                                               G; 442 T;
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Matches 157;
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                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an MS45 male tissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                             Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                          AAH76333;
                                                                   AAH76333 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 46; 50pp; English.
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    mays Ms45 male tissue-preferred regulatory region encoding DNA.

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                                                                                                                                         1275
                                                                                                                                                                                           1215 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 1274
                                                                                                                                                                                                                                                  1155 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCGTTCTTCCATCGTCC 1214
                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                  1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC 60
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                                                                                                                                                     AAGCCTTGCCTATTCTGAACCAAGAGGGATACCTACTCCCAAACAATCCATCTTACTCATG 120
                                                                                                                                      CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0;
              (first entry)
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                                                                   DNA; 1394 BP
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                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 2.4e-42;
Mismatches 0;
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Best Local :
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           WO200160997-A2
                                      Zea mays.
                                                                hybrid seed;
                                                                           Ms45; male tissue; regulatory region; transcription; male fertility;
                                                                                                     Z. mays Ms45 male tissue-preferred regulatory region
                                                                                                                                  29-OCT-2001
                                                                                                                                                                AAH76334;
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                       AAH76334 standard; DNA; 158 BP.
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                                                                                                                                                                                                                                                                           1275 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
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Similarity 100.0%;
57; Conservative (
(first entry)
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Pred. No. 2.4e-42;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-033277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                  21-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                        tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 146; DB
Pred. No. 6.1e.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146; DB 5;
No. 6.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huffman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
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(SYGN ) SYNGENTA PARTICIPATIONS
                                                                         2003-248011/24.
                                                                               Briggs SP,
T, Provart
                                                                                Cooper B,
N, Ricke
                                                                                'n
                                                                                          გ
G
                                                                                Glazebrook J,
D, Zhu T;
                                                                                   Goff SA,
                                                                                   Katagiri
                                                                                   Ŧ
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New stress-responsive nucleic acid, us responsiveness of a plant, e.g. cereal stress, salt stress or osmotic stress. acid, useful g. cereal, to for a c altering the abiotic stress Buch 86 cold

Claim 48; SEQ ID NO 17293; 89pp; English.

and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polymucleotides. Also disclosed are methods for using the polymucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polymucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polymucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, stress, osmotic stress or any of their combinations. The present seq is used in the exemplification of the invention invention relates to novel abiotic stress responsive polynucleotides des. Also disclosed are vectors, expression cassettes, host ants containing such polynucleotides. Also disclosed are

Sequence 2000 BP; 616 A; 370 C; 355 G; 659 T; 0 U; 0 Other;

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                                                                              Matches
                                                                                              Query Match
                                                                                       Local Similarity
 1879
                                       1819
                  124
                                                           64
                                                                              60;
                                                           CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA
CCTCCATGCA
                   CTTCCATGCA 133
                                      CCTTGGCTATTCCGAACCAACAGGAACACCTACTCCCCAAACAATCACGCTGACTCATGCAA
                                                                               Conservative
                                                                                       34.4%;
                                                                             Score 54; DB : Pred. No. 1.2e. 0; Mismatches
                                                                               0
                                                                                                DB 11;
                                                                               10;
                                                                                                Length 2000;
                                                                                Indels
                                                                               0;
                                                                               Gaps
                                         1878
                                                             123
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THE PROPERTY OF A CONTRACT OF AAH76336 standard; DNA; 50 AAH76336 ВP

mays Ms45 male tissue-preferred regulatory region fragment. 29-OCT-2001

(first entry)

Ms45; male tissue; regulatory region; transcription; male fertility; hybrid seed; ds.

WO200160997-A2

23-AUG-2001.

13-FEB-2001; 2001WO-US004527

15-FEB-2000; 2000US-00504487

PIONEER HI-BRED INT INC.

Albertsen MC, Fox TW, Garnaat Š Huffman ຸດ Kendall

WPI; 2001-514772/56

0

Gaps

0

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The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the M845 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment upstream of the TATA box of a green was made and the transcription of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the TATA box of a control of the present sequence represents a DNA fragment upstream of the tata o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ms45; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 BP; 18 A; 17 C; 5 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mays Ms45 male tissue-preferred regulatory region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huffman G,
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                                                                                                                                                                                                                                                                                                                                           comprising nucleotide set
the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
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ADK52131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                             Matches
                                                                                                                                  Query Match
Best Local
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                  The invention relates to detecting atopic dermatitis or psoriasis comprising assaying the levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis, comparing these levels with those of a healthy person, and determining that if the levels of indicators are higher or lower, then this indicates the disease. Also included are a reagent for detecting atopic dermatitis or psoriasis, a kit for screening for treatments, a transgenic non human vertebrate animal models for the diseases, an agent for inducing the diseases in mice and a DNA chip for assaying for the indicator genes. The method is used for treatment, detection and animal models for research of atopic dermatitis and psoriasis. The present sequence is a Mouse atopic-dermatitis/psoriasis-associated EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting atopic dermatitis or psoriasis comprises expression of an indicator gene at a rash site and person with atopic dermatitis or psoriasis.
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-214514/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitsuishi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2002; 2002JP-00229319.
14-MAY-2003; 2003JP-00136544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-2003; 2003WO-JP009999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40 BP; 14 A; 14 C; 3 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         (expressed sequence tag).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Itoh M
                                                      27
                                                                                                       66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atopic-dermatitis/psoriasis-associated
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                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV JUNTENDO.
                                                                                                                                                                                                        3267 BP;
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                                             TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ogawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.5%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                     1029 A; 658 C; 590 G; 990 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shinagawa
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                                                                                                                            20.6%;
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                                                                                                 Score 32.4; D
Pred. No. 2.5;
0; Mismatches
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Pred. No. 0.0017
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                                                                                                    56;
                                                                                                                                                  12;
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non-rash
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RESULT 9

AAH76337

standard;

DNA; 40

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29-OCT-2001

(first entry)

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вb

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Query Match Best Local S Matches 50

Similarity

31.8%; ilarity 100.0%; Conservative

Score 50; Pred. No. Mismatches

0

50;

nucleotide sequence

Claim 5; Page 47; 50pp; English.

A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.

WPI; 2001-514772/56.

Albertsen

ă,

Fox TW,

Garnaat CW,

15-FEB-2000; 2000US-00504487. 13-FEB-2001; 2001WO-US004527.

(PION-) PIONEER HI-BRED INT INC.

Claim 14; Page 32; 50pp; English.

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2774

TTCTTTTTCTCACCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 2833

3267

0;

Gaps

ΧZ

23-AUG-2001. WO200160997-A2 Zea mays. hybrid

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ACA48402/c
ID ACA484
XX ACA ACA484
XX ACA ACA484
XX ACA4
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               the 6213 antisense sequences given in the specification where expression (C) of the nucleic acid inhibits proliferation of a cell. Also included are: (C) a vector comprising a promoter operably linked to the nucleic acid (C) encoding a polypeptide whose expression is inhibited by the antisense (C) nucleic acid; (2) a host cell containing the vector; (3) an isolated (C) polypeptide or its fragment whose expression is inhibited by the activity of a gene expression is specifically binding (C) proliferation or the activity of a gene in an operon required for (C) proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway (C) identifying a compound that influences the activity of identifying a gene required for cellular proliferation or the biological pathway (C) required for proliferation, or that inhibits cellular proliferation of the proliferation of the test compound that inhibits groliferation of an occupanism acts; (9) manufacturing an antibiotic; (10) profiling a compound sactivity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent (13) identifying the target of a compound that inhibits the constitution of an organism. The antisense nucleic acids are useful for identifying the strains in preference in the proliferation of the strains or screening for homological cards remired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
08-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any one of
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DB; ABU44532.
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Trawick JD,
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2001US-0342923P.
2002US-00072851.
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Forsyth
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for homologous

The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCNN, ADRN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with concentrated with congenital heart disease, epilepsy, diseases related to

Claim 1; SEQ

ID NO 346; 27pp; English

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                                                                                                                                                                                                  Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a se of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human chemically modified disease associated
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01-SEP-2000;
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2000DE-01043826
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                                  The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,
                                                                                                                                                                                                                                                                                                                                           01-APR-1999;
18-MAY-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histone deacetylation, Currarino syndrome, diseases related with the development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or the amplification of the 350 sequences, as primer oligonucleotides for the amplification of the 350 sequences, (II) and/or their complements and as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs). Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                        WPI; 2000-587529/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCTAACCCATCTTCCAAATAAACACCC 8714
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                                                                                                                              Page 321-335; 1449pp; English
                                                                                                                                                                                                                                                  Copenhaver
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                                                                                                                                                        DNA construct comprising a plant centromere, ably inherited michrosomes which can serve a of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                CHICAGO.
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99US-0134770P.
99US-0153584P.
99US-0154603P.
                                                                                                                                                                                                                                                                                                              99US-0172493P
                                                                                                                                                                                                                                                                                                                                                                                        99US-0125219P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA; 64415
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                                                                                                                                                                                                                                                  Keith
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Pred. No. 9;
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111

Sequence 64415 BP; 18698

antibodies,

and A;

growth

factors

13554 C; 13083 G;

18980 T; 0 U; 100 Other;

Sequence

79467 BP; 18256 A; 19684 C; 20062

G;

20204

Ŧ, 0 ď;

1261 Other;

the

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RESULT 14
ADA02717
                                                         The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (ADA01482-ADA03094), and to CC arcinomal associated proteins (CAP) encoded by them. The cinvention also encompasses expression vectors and host cells comprising a CC CA nucleic acid, a polypeptide (especially an antibody) that specifically CC binds to the protein, and a biochip comprising CA nucleic acid or consequence for the sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC art canden. Many of these do not carry transduced host encogenes or consequence of the effects of proviral integration into host consequence of the effects of proviral integration into host proteoncogenes. The CA nucleic acid sequence can be used to diagnose cC carcinoma (especially breast cancer, prostate cancer, lymphoma or celukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as compensed to the represents and in screening and evaluating drug candidates. The complete sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained cc firm wino, intrinsh-American arcinoma to the complete sequence of the sequence of the proteins and antibodies are also useful as complete sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained cc.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.
                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1235; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morris DW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-DEC-2002; 2002WO-US041414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2001; 2001US-00035832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse Nfatc1 carcinoma associated gene, SEQ ID NO:1235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 79467
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Pred. No. 26;
0; Mismatches
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Query Match 19.5%; Best Local Similarity 56.4%; Matches 57; Conservative

0; Mismatches Score 30.6; Pred. No. 28;

DB 9; 44;

Length 79467;

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RESULT 15
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                                                                                                                                                                                       Query Match
Best Local S
Matches 57
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23-CCT-2001; 2001US-00094113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                                                                                                                                                                                            carcinomas, e.g. lymphomas, cancers, heaptasm, concers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Nfatcl gene
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                                                                                                                                                                                                                                                                                                                Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 283; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-239337/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morris DW, Engelhard EK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY.
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                                                                                                                                                                                       l Similarity
57; Conserv
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; neoplasm; adenocarcinoma; sarcoma; gene.
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CTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTC 151
                                                                    TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                      Score 30.6; DB 10; Length 79467; Pred. No. 28;
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                                                                                                                                                                                       Mismatches 44;
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Search completed: March Job time: 105.48 secs 5 2006, 18:11:42

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Scoring table: IDENTITY NUC Gapop 10.0 ,	Sequence:	Title:	Run on:	OM nucleic - nu
IDENTITY NUC Gapop 10.0 , Gapext 1.0	1 cgtgtcatctcacatggcatcgcacatatgtttcctgaac 157	US-10-713-381-2_COPY_1155_1311	March 5, 2006, 18:11:59; Search time 741.207 Seconds (without alignments) 9910.279 Million cell updates/sec	OM nucleic - nucleic search, using sw model

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries

Searched:

41078325 seqs, 23393541228 residues

82156650

Database: EST:*
1: gb est1:*
2: gb est2:*
3: gb est3:*
4: gb htc:*
4: gb htc:*
5: gb est4:*
6: gb est6:*
7: gb est6:*
9: gb gs81:*
10: gb gs81:*
11: gb gs81:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID No. Score Match Length DB ID CC556939 CCC566939 CCC566931 CCC56693 CCMDQ20TV C 1 157 100.0 963 9 CC656933 CCC566931 CCC56693 CCMDQ20TV 3 157 100.0 963 9 CC656933 CCC566931 CCC56693 CCC656931 CCC65693 CCC656931 CCC65693 CCC656931 CCC65693 CCC66693 CCC66693 CCC66693 CCC66693 CCC66693 CCC66693 CCC66693 CCC66693 CCC66693 CCC669	^	•	000	^	0.00	0.1	χe
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ALIGNMENTS

Query Match Best Local Matches 15	FEATURES SOURCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RÉSULT 1 CC656939/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM
/ Match 100.0%; Score 157; DB 9; Length 687; Local Similarity 100.0%; Pred. No. 2.2e-39; nes 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA 7el: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@rigr.org Seq primer: TF Class: methylation filtered.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogonaea; Zea. (bases 1 to 687) Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser; C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R. W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002) Other_GSSs: OGMD0207M Contact: Cathy Whitelaw	CC656939 687 bp DNA linear GSS 19-JUN-2003 OGWDD20TV ZM 0.7_1.5 KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence. CC656939 CC6565939.1 GI:32060231 GSS. Zea mays

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Other_GSSs: OG1AG08TH
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llarity 100.0%; F
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strain="873"
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Other_GSSs: OGWDQ20TV
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     Martienssen,R.A.
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Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; PACCAD
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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1 (baes 1 to 702)
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Whitelaw,C.A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Resnick,A., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                   CW324514 702 bp DNA linear GSS 31-OCT-2004 104 819_11477203_148_35910_078 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
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Location/Qualifiers
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methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jbedell@oriongenomics.
Plate: 819 row: c column: 1
Seq primer: SWfor Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                CW445575 296 bp DNA linear GSS 02-NOV-2004 fsbb001f170m16k0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone fsbb001f170m16, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 615 6979
Fax: 314 615 5975
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4041 Forest Park Ave,
                                                                                                                                                                       Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and Marttenssen, R.A.
                                                                                                                                                                                                                                                                                                    Sorghum bicolor (sorghum)
Sorghum bicolor
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                CW445575.1 GI:55193536
                                                                                                                                     Sorghum genome sequencing by methylation filtration procession. 3 (1), el3 (2005)
                                                                                                                                                                                                                                                                   clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 296)
                                                                                                        Contact: Bedell JA
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ass: methylation filtered
gh quality sequence stop: 702
Location/Qualifiers
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                                                                     ion Genomics, LLC
11 Forest Park Ave, St. Louis, MO 63108, USA
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314 615 6979
314 615 5975
1: jbedell@oriongenomics.com
e: fsbb001f170 row: m colu
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/mol_type="genomic DNA"
/cultivar="ATX623"
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04)"
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'clone="11477203"
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Pred. No. 3.9e-09;
0; Mismatches 5
    column: 16
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                                                                                                                                                                                                                                                               The Institute for Genomic Research
Department of Eukaryotic Genomics, TI
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 101-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT-CCATCTTACTCATGCA 122
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genomic survey sequence.
CE588104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (dog)
Canis familiaris
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidas
                                                                                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 636)
Kirkness, B.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CE588104
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                                                                                                                                                                                                                                              ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared from purified nuclei was randomly—sheared, end-repaired, size fractionated to enrich for the 0.5 to be fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
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clone="fsbb001f170m16"
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cultivar="ATx623"
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mol_type="genomic DNA"
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                                                          /clone lib="Dog Library"
/note="Site 1: BstXI; Li
peripheral blood"
                                                                                                                /organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
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            24.1%;
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Pred. No. 0.00042;
0; Mismatches 10
            Score 37.8;
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                                                                                   Libraries
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              DB 10;
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            Length 636;
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                                                                                                                                                                                                                                                                             333 TATTTTTTCCCAGTTCAAGGCATCCTTGTTTGGACCCAAGGGTATACCTCATTTTTAAAA
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sequence.
AG366773
AG3667731 GI:47977978
GSS.
Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
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G11-25n6 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.
                                                                                                                         Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlueter, T., Hermanns, J., Weindel, M., Henrich, J. and Loebbert, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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                                                                                                                                          AG366773
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                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9615"
/tissue_type="kidney"
/dev_stage="adut"
/dev_btage="dH10B"
/lab_host="DH10B"
/clone_lib="DG11-kidney"
/note="Organ: kidney; Vector: Dog pBluescript LION"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Canis familiaris"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
/strain="Beagle"
                                                                                                                                                                                                                                                                                                                                                   24.1%;
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                                                                                                                                                                                                                                                                                                                                     Score 37.8; DB 7;
Pred. No. 0.49;
0; Mismatches 47;
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0; Mismatches
                                                                                                                         DNA,
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clone:MSMg01-170B12.TJ,
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R.Site 2
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Oryza coarctata (Porteresia coarctata)
Oryza coarctata
Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 24.1%;
l Similarity 51.9%;
69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-NOV-2003) Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (Picker), Tokohama, Kanagewa, 230-0045, Japan (B-mail:hattori@ggc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC Clones are derived from the mouse BAC library MSMg01.
                                                                                                                                                                               CZ727957 874
OC_Ba0055L24.f OC_Ba Oryza
5', genomic survey sequence.
CZ727957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library availability, please contact Kuniya Abe Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contribution of Asian mouse subspecies Mus musculus molossinus genomic constitution of strain C57BL/6J, as defined by BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., K
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 14 (12), 2439-2447 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATATGTTTCCTG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACATNAATAACNCCCCCCNANNAAACCANNANAACCCCCGCAATTTTTTNANAANNATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACC 81
                                                                                                                                                                                                                                                                                                                                                                                                  CAAACTTTTTTTG 587
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/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mixture of kidney and
/clone_lib="MSMg01 Mouse Male BAC Li
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Ba Oryza
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BAC Library"
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> OC__Ba0055L24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                778 CCTTGGCTATTCCGAACCAACAGG-CACCTACTCTCAAAACATCACGCCGACTCATGCAA 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                             Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Komo, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura Ohno, M., Okazaki, Y., Okido, T., Saico, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shlbata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB505306 mRNJ
BB505306 RIKEN full-length enriched, 10
female mammary gland Mus musculus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: TAA TAC GAC TCA CTA TAG GG Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 874)
Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 520 626 9595
Fax: 520 621 1259
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                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                   BB505306.2 GI:16442791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
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                                                                                                                                                                                                                                                                                                                                            musculus
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ry ror Genome Exploration Research Group, RIKEN Genomic Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="OC_Ba"
/note="Vector: pAGIBAC1;
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/db_xref="taxon:77588"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Oryza coarctata"
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                                                                                                                                                                                                                                        Carninci, P.
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                                                           this sequence version replaced gi:9514268.
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1ed, 10 days lactation, ad
1s cDNA clone D730002G06, #
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit on further details
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RIKEN integrated sequence analysis (RISA) system -384-format
RIKEN integrated with 384 multicapillary sequencer. Genome Res.
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                                           cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                               GAGAGAGAGAGCGGCGCACTCGAGTTTTTTTTTTTTTTVN 3'), cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
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/mol_type="mRNA"
/db_xref="taxon:10090"
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dev_stage="10 days lactation, adult"
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and sequenced in Mouse Genome Encyclopedia
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Matches Query Match Госат 195 87 GATACCTACTCCCAAACAATCCATCTTACTCATGCAACCTTCCATGCAAACACGCACATAT 146 27 TGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAG 86 67; Similarity TTCTTTTTCTCCCCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 254 Conservative 21.7%; Score 34; DB: Pred. No. 8.3; 0; Mismatches 0, Length 700; 55; Indels 0, Gaps

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                                                                  CL026582 1677 bp DNA CH216-23G24_Sp6.1 CH216 Xenopus tropicalis CH216-23G24, genomic survey sequence.
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Institute of Molecular and Cell Biology
El Biopolis Drive, Singapore 138673
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Holocephali; Chimaeriformes; Callorhinchidae; Callorhinchus.
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Callorhinchus milii
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CW871670
Xenopus tropicalis (western clawed frog) Xenopus tropicalis
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CL026582.1 GI:40470443
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Venkatesh, B., Tay, A., Dandona, N., Patil, J.G.
A compact cartilaginous fish model genome
Curr. Biol. 15 (3), R82-R83 (2005)
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65 6779 1117
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genome shotgun sequences (
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/clone lib="Whole-genome shotgun library
shark (aka elephant fish)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Callorhinchus milii"
/mol_type="genomic DNA"
/db_xref="taxon:7868"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="Male"
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Local Similarity
Hominidae; Homo.

E 1 (bases 1 to 440)

S NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP)

Tumor Gene Index

Unpublished (1997)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Cen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889 TCTTCCAT 896
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Insert Length: 175000 Std Error:
Seg primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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Kremitzki,C., Carter,J., McPherson,J., Warren,W., Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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Washington University School of Medicine
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AI744861
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Mammalia; Eutheria;
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/mol types"genomic DNA"
/strain="Nigerian frog"
/db xref="taxon:8364"
/clones"CH216-23G24"
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/clone_lib="CH216"
/note="Vector: pTARBAC2.1; (
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Pred. No. 1:
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IMAGE:2218451 3',
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'n

FEATURES

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319 TCCATCTTAATTAAACAGCGTCGATGTCTGCCTAGATATCTGTTTCCCT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 TCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 CTTTGGCCAGCAAACTAGTATATCATATTCCTCCCCAAAGCAACACCTCCTACTTTATTT 318
                Naming Conventions: EST name is generated by the concatenation of the dGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

Poly-A: Based upon the presence of a run of 14 or more T residues
                                                                                                                                                                                                                 Email: cdna@jgi.psf.org
Email: cdna@jgi.psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
cDNA Library Preparation: Richard M. Harland Laboratory, University
                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2004)
Other ESTs: JGI XZG22009.fwd
Contact: Lindquist, E.A., Rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 CTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAA 105
                                                                                                                                           http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CX446438
GI XZG22009.rev NIH XGC_tropGas7 Xenopus tropicalis IMAGE:7537449 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                     OOB Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CX446438.1 GI:57262270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Srokstein, P. and Lindquist, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richardson, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibia; Batrachia; Anura; Mesobatrachia;
(enopodinae; Xenopus; Silurana.
(bases 1 to 648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/hage.html
Seq primer: -40UP from Gibco

    California, Berkeley
    A Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
    Lone Distribution: I.M.A.G.E. Consortium/LLNL:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 411.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Institute Xenopus tropicalis EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=Worgan: ovary; Vector: pCMV-SPORT6; Site 1: Site 2: NotI; Cloned unidirectionally. Primer: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="NCI_CGAP_Ov23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="tumor, 5 pooled (see description)"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE: 2218451"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32.8; DI
Pred. No. 18;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                     Richardson, P.
this clone was polyadenylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 07-JAN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
CW558661/c
                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                  COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                          source
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ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE

AUTHORS TITLE RESULT 14 CX446438/c

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ORIGIN

Query Match Best Local : Matches 6:

DEFINITION

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586 TTTGAATTATGAAAAGGCCATCTCCCATAGACTCCATTTTAGGCAAGTAATTTCCATTTT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 AAAAAGTATTTTTTTCC 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AACACGCACATATGTTTCC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 ГСТБААССАВБАББАТАССТАСТСССАВАСЬАТССАТСТТАСТСАТБСВАСТТССАТБСВ 133
                                                                              Plate: 0080 row: B column: 07
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza australiensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                        Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CW558661 740 bp DNA
OA_ABa0080807.f OA_ABa Oryza australiensis
OA_ABa0080807.f', genomic survey sequence.
                                                                                                                                                FORWARD: TAA TAC GAC TCA CTA TAG
                                                                                                                                                                                                                                                                                                                                                  Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CW558661
                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CW558661.1 GI:54424196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 185 POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The resulting Poly-T sequence has Plate: XZG 0229 row: b column: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 740)
                                                                                                                                                                                                  PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                    rwing@genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu, Y.
organism="Oryza australiensis"
| mol_type="genomic DNA"
                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NIH_XGC_tropGas7"
/note="Vector: pCS108; Site 1: SalI; Site 2: NotI;
Gastrula library constructed by Russell B. Fletcher in R.
Harland's lab using poly A RNA and oligo dT primers
Invitrogen SuperScript Plasmid System for cDNA Synthesis
and Cloning). SalI [5' end) -NotI [3' end) cDNA was
interted into vector pCS108
[http://mcb.berKeley.edu/labs/harland/pages/plasmids.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db xref="taxon:8364"
/clone="tMAGE:7537449"
/tissue_type="whole embryo"
/tissue_type="whole embryo"
/day_stage="Gastrula (st. 10.5-12.5)"
/lab_host="E. coli XLI-Blue derivative, Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                            Muller, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Stum, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryzeae;
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Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       ., Yost,D., Rao,K., Luo,M., Jetty,R., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza.
                                                                                                                                                     CCA
                                                                                                                                                                         ရှ
                                                                                                                                                                                                                                                                              AZ 85721-0036,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic clone
                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 22-OCT-2004
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                     Sequence 1, Appli
Sequence 2, Appli
Sequence 16073, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 14712, A
Sequence 14713, A
Sequence 14712, A
Sequence 117101,
Sequence 117101,
Sequence 11740, A
Sequence 11740, A
Sequence 16740, A
Sequence 17440, A
1813, Ap
1413, Ap
10489, A
2, Appli
3747, Ap
3680, Ap
4003, Ap
2556, Ap
23, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,499

PLIUM DATE: CONCURRENTLY HEREMITH

CLASSIFICATION: 800
        Query Match
                                                                                                                                                                                                                                                             TELEPXX: (515) 248-4800
TELEPXX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 bar-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                MOLECULE TYPE: DNA (genomic)
-880-499-1
                                                                                                                                                                                     LENGTH: 1394 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Johnston
3: Iowa
FRY: USA
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                100.0%; Score 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-13779
US-09-949-016-13779
US-09-949-016-1776
US-09-949-016-17130
US-09-949-016-17130
US-09-949-016-17130
US-09-949-016-13037
US-09-949-016-13037
US-09-949-016-13037
US-09-949-016-13038
US-09-949-016-13039
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149-016-17368
149-016-14091
149-016-13779
149-016-17576
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                     Length 1394;
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Sequence
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13779, A
13779, A
13779, A
17576, A
17576, A
1999, A
1999, A
11999, A
11999
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Post_processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued Patents NA:*

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2: /cgn2 6/ptodata/1/
3: /cgn2 6/ptodata/1/
4: /cgn2 6/ptodata/1/
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/ECTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Ba_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

1303057 seqs, 888780828 residues

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Title: Perfect score:

US-10-713-381-2_COPY_1155_1311 157

cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157

Run on:

nucleic search, using sw model

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration

Ltd.

March 5, 2006, 21:54:12;

Result No.

.Query Match Length DB

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Description

SUMMARIES

US-08-880-499-1 US-08-880-499-2 US-09-949-016-16073 US-09-543-681A-1081

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3 US-09-557-884-1
3 US-09-643-990A-1
3 US-09-18-865-1
3 US-09-18-865-1
3 US-09-949-016-147/2
3 US-09-949-016-15502
3 US-09-949-016-15502
3 US-09-949-016-151201
3 US-09-949-016-191201
3 US-09-949-016-16740
5 US-09-97-166-16740
5 US-09-97-166-16740
5 US-09-97-166-17413
5 US-09-97-166-17413
5 US-09-97-167-10413
5 US-09-710-279-1813
5 US-09-710-279-3680

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US-08-880-499-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 60375
                                                                                                                                             Matches 157;
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                               TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Box 100
CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
1215
                                                                     1155
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                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC
                  AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                          Application US/08880499
AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                     CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 1214
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(515) 248-4844
                                                                                                                                             Conservative
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Huffman, Gary A.
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                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                   single
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) 248-4844
NO: 2:
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                                                                                                                                                            100.0%; Score 157; DB 3; 100.0%; Pred. No. 9.4e-44;
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                                                                                                                                                                           Length 1394;
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; OTHER INFORMATION: n = A,T,C or US-09-949-016-16073
                                                                                                                      ; ORGANISM: Proteus mirabilis US-09-543-681A-1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-543-681A-1081/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-16073/c
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT FILING NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 16073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16073
                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1081, App
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                           Best Local
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(38513
                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 385136
                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253848 TCCATTTACTCCCACCACACACACATTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 CTCATGCAACTTCCATGCAAACACGCACATATGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA 114
35 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA 94
                                                                                                                                                                                      1185
                                        l Similarity
50; Conserv
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                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09543681A
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                                                           18.9%;
                                      Score 29.6; DB Pred. No. 3.4; 0; Mismatches
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Pred. No. 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                              DB 3;
                                          34;
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                                                                                Length 1185;
                                        Indels
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940 CAACAATTTGTTTTTGTCCACCAGAAAGACCTAACCCATTTTCTCCCCAAGGACATATCTA 881

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RESULT 6
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                          677275 ACTITAAAITCAGCCTGCTTGCTTGCTATTGCATTTGCATTAAATGCAAGCATAGCCT
                                                                                                                                                                                677215
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9110 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fleischmann Fitte OF INVENTION:
                                                                                                                                         132 CAAACACGCA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            880 ATCCCCTAGGATGCTTTTAATAA 857
                                                                                                                                                                                                                                                                                                   12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 CTCCCAAACAATCCATCTTACTCA 118
                                                                                                                                                                                                                     72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                  CAACCAACCA 677146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3 1/2 inch diskett COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS v6.22 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09557884
                                                                                                                                                                                APPLICATION NUMBER: 08/476,102 FILING DATE: JUN-5-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                        18.6%;
ilarity 51.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFAX: 301-309-8439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann et al.

IVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inch diskette
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US-09-643-990A-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 67; Conserv
Patent No. 6846651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                  677155 CAACCAACCA 677146
                                                                                                                                                                                                                                                                       APPLICANT: Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 132 CAAACACGCA 141
                                                                                                                                                                                                                                                                                                              72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                        12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
                  INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville,
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/426,787 FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/487,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 301-610-57,90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                              Application US/10158865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%;
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; Pred. No. 63;
0; Mismatches
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FILE REFERENCE: PB186P2C1D1
CURRENT APPLICATION NUMBER: US/10/158,865
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR PILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patent
SEQ ID NO 1
LENGTH: 1830121
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (9921) . (9921)
OTHER INFORMATION: n equi
                                FEATURE:
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LOCATION: (44416)...(44416)
OTHER INFORMATION: n equal
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals
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LOCATION: (36551)...(36551)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
OTHER_INFORMATION: n equals
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OTHER INFORMATION: n equals
                                                              NAME/KEY: misc_feature
LOCATION: (45732)..(45732)
OTHER_INFORMATION: n equals
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LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a,t,
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LOCATION: (36543)..(36543)
DTHER_INFORMATION: n equals
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LOCATION: (4747)...(474
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JOCATION: (44905)..(44905)

OTHER INFORMATION: n equals
OCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc feature
LOCATION: (80074)..(80024)
OTHER INFORMATION: n equals
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equals
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LOCATION: (51805)...(51805)
OTHER INFORMATION: n equals
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals
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LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals
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LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals
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LOCATION: (100091)..(100091)
OTHER_INFORMATION: n equals
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (55369)...(55369)
OTHER INFORMATION: n equals
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals
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LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals
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NAME/KEY: misc feature
LOCATION: (119924)..(119924)

OTHER INFORMATION: n equals
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LOCATION: (102696)..(102696)
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LOCATION: (122167)..(122167)
OTHER_INFORMATION: n equals
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AME/KEY: misc_feature
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RESULT 8
US-09-949-016-14712/c
; Sequence 14712, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
   Applicant: VENER, J. Craig et al.
; Applicant: VENER, J. Craig et al.
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LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (140398)..(140398
OTHER INFORMATION: n equals
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LOCATION: (131340)..(131340)
OTHER_INFORMATION: n equals a,t,c,
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OTHER INFORMATION: n equals a,t,c,
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (145058)..(145058)
OTHER_INFORMATION: n equals a,t,c,
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LOCATION: (142750)..(142750)
DTHER_INFORMATION: n equals
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LOCATION: (139910)..(139910)
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OCATION: (147197)..(147197)
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LOCATION: (145942)...(145942)
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.OCATION: (145171)...(145171)
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l Similarity 51.5%;
67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      Score 29.2;
Pred. No. 63
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US-09-949-016-14712
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; Sequence 14713, Application US/09949016
                                     RESULT 10
US-09-949-016-15502
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; ORGANISM: Human
US-09-949-016-14713
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Best Local S
Matches 45
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 14712
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SEQ ID NO 14713
Sequence 15502, Application US/09949016 Patent No. 6812339
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Best Local
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-09-08
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CL001307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 CTCATGTAACAT 284
                                                                                                             295 CTCATGTAACAT 284
                                                                                                                                            115 CTCATGCAACTT 126
                                                                                                                                                                                  355 TCATCCAATAGTTTCCACTACTAATCCATGATGGAACTGAGTACTAATCAAGCCAATATT 296
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LING DATE: 2000-09-08
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Pred. No. 27;
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Pred. No. 27;
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GENERAL INFORMATION:

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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-09

NUMBER OF SEQ ID NOS: 207012

SOPTWARE: FASCSQ for Windows Version 4.0

SEQ ID NO 15502

LENGTH: 11022
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; ORGANISM: Human
US-09-949-016-17447
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US-09-949-016-17447
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                                                                                                                                                                      Matches
                                                                                                                                                                                                               Query Match
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTIO
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                    ENGTH: 41815
                                                                                                                                                                                     Local Similarity
33118
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                                       122 AACTTCCATGCAAACACGCACATA 145
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                                                                                                                        62 AGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATT 74
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  ATGTCACATAGAGACATGCATGTA 33141
                                                                                   AGACATGCAGATTCACACACATCCGCATAGCTGCTCCTACGGATCCCTGGTCACTCATTC 33117
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Pred. No. 43;
0; Mismatches 3
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Pred. No. 27;
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RESULT 12

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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 191201
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; ORGANISM: Human
US-09-949-016-14149
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GENERAL INFORMATION:
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SEQ ID NO 14149
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GENERAL INFORMATION:
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Best Local Similarity
Matches 62; Conserv
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CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-01-1755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
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SOFTWARE: FastSEQ for Windows Version
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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TYPE: DNA
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                JENGTH: 11490
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                                                                                       5642 CAGGGCCTCTGCTTCCCTGCCCCTCCCCCTGCCCCCACCTCACCAGGAGGAAGCCCACGC 5583
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                                         98 CCAMACANTCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAA 156
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  CCTTGCACACCTGATGCCACATCCGCTTGAGTGGCAGGCGAGTGAAGATGTTGCCCCAAA
                                                                                                                                  CCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTC 97
                                                                                                                                                                              Conservative
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; Pred. No. 11;
1; Mismatches
                                                                                                                                                                           Score 27.8; DE Pred. No. 32; 0; Mismatches
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09-949-016-16740

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; OTHER INFORMATION: Description of Artificial Sequence; No. 6846621e; OTHER INFORMATION: synthetic construct
US-09-937-862B-37
                                      Query Match 17.6%; Score 27.6; I Best Local Similarity 55.1%; Pred. No. 15; Matches 54; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.7%;
Best Local Similarity 59.5%;
Matches 47; Conservative
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-09-949-016-16740
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                                                                                                                                                                                              TYPE: DNA
DRGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                            JMBER OF SEQ ID NOS: 89

JETWARE: FastSEQ for Windows Version 4.0

ON O 37
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LE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

LE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/241,755 FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 CCATGCAAACACGCACATA 145
53 CATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 TGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 TGTCAACCGTGATCCAACAGTATAATTAGTTCTTAGGAATTCCTCTCTCACAGGTAACTA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7, Application US/09937862B
6846621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATION NUMBER: 60/231,498
G DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                TION NUMBER: PCT/US00/07828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                              JMBER: 60/127,464
1999-03-31
                                                                                                                                                                                                                                                                                                                                                                                            2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPING OF HUMAN ENTEROVIRUSES
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Pred. No. 35;
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                                                                                 _ DB 3; Length 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 14952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                      Gaps
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Search completed: March 5, 2006, 22:36:28 Job time: 46.8947 secs

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Run on: OM nucleic - nucleic search, using sw model March 5, 2006, 23:29:31; Search time 225.751 Seconds (without alignments) 5750.985 Million cell updates/sec. GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. 大きなないで 子

Title:
Perfect score:
Sequence: US-10-713-381-2_COPY_1155_1311 157 1 cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157

Searched: IDENTITY NUC
Gapop 10.0 , Gapext 1.0 9793542 seqs, 4134689005 residues

Scoring table:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

19587084

Database : Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA_Main:*

1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	321	20	19	18	17	16	15	14	13	12	c 11	c 10	9	а 8	c 7	6		4	ω	N	_		Result
29.8	30 30	30	30	30.2	30.2	30.2	30.4	30.6	30.6	30.6	30.8	30.8	31.4	31.6	32.2	40	50	146	157	157	157	atote	
19.0	19.1	19.1	19.1	19.2	19.2	19.2	19.4	19.5	19.5	19.5	19.6	19.6	20.0	20.1	20.5	25.5	31.8	93.0	100.0	100.0	100.0	Match	Query
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US-09-925-065A-285326	US-10-027-632-170626	US-10-027-632-170626	US-10-713-381-4	US-10-501-282-6651	US-10-501-282-2923	US-09-925-065A-153052	US-10-317-273-11	US-10-052-482-223	US-10-027-632-244811	US-10-027-632-244811	US-10-437-963-1496	US-09-925-065A-778732	US-09-925-065A-871704	US-10-282-122A-36272	US-10-674-124A-9081	US-10-713-381-6	US-10-713-381-5	US-10-713-381-3	US-10-713-381-2	US-10-713-381-1	US-10-713-381-9		•
Sequence 10490, A Sequence 285326,		Sequence 170626,	Sequence 4, Appli	Sequence 6651, Ap	Sequence 2923, Ap	Sequence 153052,		Sequence 223, App				Sequence 778732,	Sequence 871704,		306	Sequence 6, Appli	Sequence 5, Appli	ω	N	Sequence 1, Appli	Sequence 9, Appli	Description	-

RESULT 2 US-10-713-381-1 ; Sequence 1, Application US/10713381 ; Publication No. US20040221331A1

ALIGNMENTS

QY 121 CAÁCTTCCATGCAACACGCACATATGTTTCCTGAAC	Qy 61 AAGCCTTGCCTATTCTGAACC	QY 1 CGTGTCATCTCACATGGCATACTACATGCTTGT	Query Match 100.0%; i Best Local Similarity 100.0%; i Matches 157; Conservative 0;	RESULT 1 US-10-713-381-9 US-10-713-381-9 US-10-713-381-9 JEQUENCE 9, Application US/10713381 Publication No. US20040221331A1 JENERAL INFORMATION: APPLICANT: ALBERTSEN, MARC C. APPLICANT: GARNART, CARL W. APPLICANT: HUFMAN, GARY APPLICANT: HUFMAN, GARY APPLICANT: KENDALL, TIMMY L. TITLE OF INVENTION: USING SAME TITLE OF INVENTION: USING SAME FILLE REFERENCE: 578R CURRENT APPLICATION NUMBER: US/10/713,381 CURRENT FILING DATE: 2003-11-14 PRIOR APPLICATION UNMER: 08/880,499 PRIOR FILING DATE: 1997-06-23 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 9 LENGTH: 255 TYPE: DNA JORGANISM: Zea mays US-10-713-381-9
CATATGTTTCCTGAAC 157	AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACCAATCCATCTTACTCATG 120	CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60	Score 157; DB 8; Length 255; Pred. No. 2.1e-43; Mismatches 0; Indels 0; Gaps 0;	81 PREFERRED REGULATORY REGION AND METHOD OF 0/713,381

GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD TITLE OF INVENTION: WISING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10713381 Publication No. US20040221331A1
                                                                                                                                         Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 157; Conservative 0;
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                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARY
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                      ENGTH: 1394
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61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                    CAACTICCATGCAAACACGCACATATGTTTCCTGAAC 157
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                                                                                                                                           Score 157; DB 8;
Pred. No. 3.8e-43;
); Mismatches 0;
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-3
; SOFTWARE: PatentIn Ver. 2; SEQ ID NO 5; LENGTH: 50; TYPE: DNA; ORGANISM: Zea mays US-10-713-381-5
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US-10-713-381-5
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Best Local Similarity
Matches 157; Conserv
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                                                                                                                     APPLICANT: ALBERTSEN, MARC C.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFWAN, GARY
APPLICANT: HUFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
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99.4%;
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Pred. No. 1e-39;
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/674,124A
CURRENT FILING DATE: 2003-09-26
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                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 10/257,511
PRIOR FILING DATE: 2003-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-674-124A-9081/c
                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
LITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
FILE REFERENCE: ORIN-003CIP
OTHER INFORMATION: chr5.fa.O7frz.139538206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                           GANISM: Homo sapiens
                                                                                                                                                                                                                                             APPLICATION NUMBER: JP2000-112699 FILING DATE: 2000-04-13
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/JP00/0762: FILING DATE: 2000-10-30
                                                                                                                                                                        APPLICATION NUMBER: JP2002-383869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/713,381 FILING DATE: 2003-11-14
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                                                                                                                                  SEQ ID NOS: 27110
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No. US20040221331A1
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                                                                        Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DET 6 10-282-122A-36272/c
10-282-122A-36272, Application US/10282122A
equence 36272, Application US/10282122A
ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Distance between a terminus base of telomere of the OTHER INFORMATION: chromosomal short arm and 5'-terminus of this OTHER INFORMATION: sequence: 128437212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence: 250186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Located on chromosome
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                                                                                                                                                 APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                      CATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATION NUMBER: 60/191,078
DATE: 2000-03-21
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Yamamoto, Robert
Forsyth, R.
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DATE: 2000-0
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IG DATE: 2003-02-20
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                                                                                                                                                                                                                          ON NUMBER: 60/257,931
                                                                                                                                                                                                                                                               ON NUMBER: 60/253,625
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lio, Carlos
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Pred. No. 1.6;
0; Mismatches
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; Sequence 778732, Application US/09925065A
; Publication No. US20050228172A9
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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US-09-925-065A-871704
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                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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Matches
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ORGANISM: Homo sapiens
-09-925-065A-871704
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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llarity 60.2%;
Conservative
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Pred. No. 3.4;
1; Mismatches
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Pred. No. 4.
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Mismatches
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1496
LENGTH: 1122
Type: DNA
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; ORGANISM: Homo sapiens
US-09-925-065A-778732
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 778732
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Publication No. US20040123343A1
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Best Local Similarity
                                                                                                                                   Best Local Similarity Matches 56; Conserv
                                                                                                                                                                 Query Match
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                    ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: PAT_MRT4530_101357C.1
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                                                                 234 AACACTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 CAMAÇACGÇA 141
                             120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                60 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
TCAGATCCACAAATCGCACCCTCCCATATCTGCTGAAC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTATAAATGATAAATTTTTCTATACACATACAGTTTTTCTACCCCATATTATCTTTCCTA 235
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                                                                                                                                   Conservative
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                                                                                                                                                19.6%;
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Pred. No. 5.
                                                                                                                                                   Score 30.8;
Pred. No. 7
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                                                                                                                                   Mismatches
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                                                                                                                                                                     DB 7;
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                                                                                                                                                                     Length 1122;
                                                                                                                                     Indels
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                                                                                                                                   Gaps
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RESULT 12 US-10-027-632-244811 · Sequence 244811, Application US/10027632

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RESULT 13
JS-10-027-632-244811
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Publication No. US20030204075A9
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Best Local
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                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR STITMS CAMPAGE US 60/198,676
                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                         PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERAL INFORMATION:
PEPLICANT: Wang, David G.
RITLE OF INVENTION: Identification and Mapping of Single Nucleotide
RITLE OF INVENTION: Polymorphisms in the Human Genome
                                        APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 ATTTTCTTCCCAA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      440 TCTGCTCCCTACCTTTAAAGATTCCATGGAAGTCCTACAAAATCCCATAGCACACTGAAC 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 ACATGCATITCTAGCITTTCGATTTTGCTCATCTTGCTGGAGGTACTTTTTCTAGATTCA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 TATGTTTCCTGAA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GAGGATAÇCTAÇTCCCAAACAATÇCATCTTACTÇATGÇAACTTÇCATGCAAAÇAÇGÇACA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 ACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
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LING DATE: 2000-04-20
PPLICATION NUMBER: US 60/193,483
LING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATION NUMBER: US 60/167,363
G DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATION NUMBER: US 60/218,006
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ON NUMBER: US 60/146,002
                             1999-09-28
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Pred. No. 6.3;
0; Mismatches
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SOPTWARE: Pateman, SEQ ID NO 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Engelhard, Eric
APPLICANT: MOXIS, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: A-71087/RmS/DCF
CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (1377)..(13370)
OTHER INFORMATION: "n" at positions 13273 to 13370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 241
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                            NAME/KEY: misc feature OCATION: (46579)..(46
                                                                                                       AME/KEY: misc_feature
OCATION: (30751)..(30
                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (20762)..(20
                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (10089)..(10
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (5502)..(552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ME/KEY: misc_feature
CATION: (4099)..(436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGANISM: Mus musculus
INFORMATION: "n" at positoins 46759 to 46772 can be any base
                                                                                                                                                                                                                                                                                                      ION: (10089)..(10620)
___INFORMATION: "n" at positions 10089 to 10620
                                                                                                                                                                                                                                                                                                                                                                            ION: (5502)..(5521)
_INFORMATION: "n" at positions 5502 to 5521 can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 0
                                                                        ON: (30751)..(30916)
INFORMATION: "n" at positions 30751 to
                                                                                                                                             ON: (20762)...(20701)
INFORMATION: "n" at positions 20762 to 20781 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: "n" at E:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 ATTTTCTTCCCAA 512
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b. US20040072264A1
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                            (46772)
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51.9%; Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                          positions 4099 to 4369 can be any base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09/798,586
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                                                                             30916 can
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (77382)..(77401)
; OTHER INFORMATION: "n" at positions 77372 to 77401 can be any base US-10-052-482-223
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US-10-317-273-11
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APPLICANT: Tamara Balac Sipes
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL RIBOSOMAL PROTEIN L13 EXPRESSION
FILE REFERENCE: RTS-0478
CURRENT APPLICATION NUMBER: US/10/317,273
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 159
SEQ ID NO 11
                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/10317273
Publication No. US20040110158A1
GENERAL INFORMATION:
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Best Local Similarity 56.4
Matches 57; Conservative
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 11220
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 11154, 11155, 11156, 11157,
LOCATION: 11163, 11164, 11165, 11166,
LOCATION: 11171, 11172, 11173, 11174,
LOCATION: 11179, 11180, 11181, 11182,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 11121, 11122, 11123, 11124, LOCATION: 11130, 11131, 11132, 11131, LOCATION: 11138, 11139, 11140, 11141, LOCATION: 11146, 11147, 11148, 11149, LOTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 52001
TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 11187, 11188, 11189, LOCATION: 11197, 11198, 11199,
LOCATION: 11196, 11197, 11198, 11199,
LOCATION: 11204, 11205, 11206, 11207,
LOCATION: 11212, 11213, 11214, 11215,
                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n
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                                                                                                                                                                                   Local Similarity
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                                           110
                                                                                                                                                                   49;
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                       TCTTACTCATGCAACTTCCA 129
                                                                                 TTTCTTTTTCTAAAACTGAAATTCCATGAAAAAAGAGAATATCAATTTTAAAACTACCCA
                                                                                                           TTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGGATACCTACTCCCAAACAATCCA 109
TCTTTCTCAGCAAACTTCTA 20134
                                                                                                                                                                   Conservative
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                                                                                                                                                             19.4%; Score 30.4; DB 7; Length 52001; 61.2%; Pred. No. 39; tive 0; Mismatches 31; Indels 0;
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, 11167, 11168,
, 11175, 11176,
, 11183, 11184,
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, 11134, 11135,
, 11142, 11143,
, 11150, 11151,
                                                                                                                                                                                                                                                                                                                                                                        11191, 11192, 11193, 11194, 11200, 11201, 11202, 11203, 11208, 11209, 11210, 11211, 11216, 11217, 11218, 11219
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, 11169, 11170,
, 11177, 11178,
, 11185, 11186
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Search completed: March 6, 2006, 03:55:15 Job time : 226.751 secs

GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Title:
Perfect score:
Sequence: Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Run on: Database : Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: Searched: OM nucleic - nucleic search, using sw model March 6, 2006, 01:58:03 ; Search time 163.89 Seconds (without alignments) 2100.307 Million cell updates/sec 7218535 seqs, 1096242582 residues US-10-713-381-2_COPY_1155_1311 157 1 cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157 Published Applications NA New: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:* nn2-6/ptodata/2/pubpna/USO) NEW PUB.seq: *
nn2-6/ptodata/2/pubpna/USO) NEW PUB.seq: *
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nn2-6/ptodata/2/pubpna/USIO NEW PUB.seq: *
nn2-6/ptodata/2/pubpna/USIO NEW PUB.seq: *
nn2-6/ptodata/2/pubpna/USII NEW PUB.seq: *
gnn2-6/ptodata/2/pubpna/USII NEW PUB.seq2: *
gnn2-6/ptodata/2/pubpna/USII NEW PUB.seq2: *
gnn2-6/ptodata/2/pubpna/USII NEW PUB.seq2: *
gnn2-6/ptodata/2/pubpna/USII NEW PUB.seq4: *
gnn2-6/ptodata/2/pubpna/USII NEW PUB.seq4: * 14437070

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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17.8 17.8	18.1	18.1 18.1	18.3 18.1	18.3 18.3	18.7	19.0	19.0 19.0	19.4 19.2	19.6	20.0	Query Match
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Sequence 173193, Sequence 32050, A	Sequence 33980, A Sequence 724023,	Sequence 33976, A Sequence 33977, A	Sequence 47517, A Sequence 845392,	Sequence 805392, Sequence 47517, A	Sequence 209, App		Sequence 285326, Sequence 285327,	Sequence 13, Appi Sequence 153052,	Sequence 185, App		Description

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27.4	27.6	27.6	27.6	27.8	27.8	27.8	27.8	27.8	27.8	27.8	27.8	28	28	28	28	28	28	28	28	28	28	28	28	28	
17.5	17.6	17.6	17.6	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.7	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	17.8	
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sequence 95		Sequence 55	Sequence 55	Sequence 23	Sequence 58	Sequence 58	Sequence 37	Sequence 37	Sequence 75	Sequence 94	Sequence 42	Sequence 39	Sequence 39	Sequence 30		Sequence 68	Sequence 68	Sequence 68	Sequence 68	Sequence 55	Sequence 55	Sequence 33		Sequence 32	
95915, A	68127, A	55178, A	55178, A	23, App1	58624, A	•	37809, A	37809, A	757513,	945788,	427091,	39884, A	-	-	•	686354,	686353,	686352,	686351,	553736,	553735,	33979, A	•	-	

ALIGNMENTS

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Qy 64 CCTTGCCTATTCTGAACCAAGAG 86	274 64	Query Match 20.0%; Score 31.4; DB 6; Length 565; Best Local Similarity 60.2%; Pred. No. 2.7; Matches 50; Conservative 1; Mismatches 32; Indels 0; Gaps 0;	; TYPE: DNA ; ORGANISM: Homo sapiens US-09-925-065A-871704	FILING DATE: 2001-05-09 R OF SEQ ID NOS: 957086	APPLICATION NUMBER: US	FILING DATE: 2000-11-30 APPLICATION NUMBER: US	; PRIOR FILING DATE: 2000-10-24 ; PRIOR APPLICATION NUMBER: US 60/252,147	; CURRENT FILING DATE: 2001-08-08; PRIOR APPLICATION NUMBER: US 60/243,096	APPLICATION N	; TITLE OF INVENTION: Identification and mapping of Single ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome	CANT: Wang, David G.	Publication No. US20040181048A1	RESULT 1 US-09-25-065A-871704 DE-09-25-065A-871704 Deption US/00025065A

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US-09-925-065A-778732/c

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RESULT 3
US-11-117-187-185
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; ORGANISM: Homo sapiens
US-09-925-065A-778732
                                                 US-11-117-187-185
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PRIOR FILING DATE: 2000-10-24
PRIOR PELICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-30
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
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Query Match
                                                                                                                                                                                                                                                                    APPLICATE: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PREUSS, APPLICANT: COPENH
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                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1 EQ ID NO 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                            NAME/KEY: modified base LOCATION: (9960)..(2114) OTHER INFORMATION: N =
                                                                                                                                       FEATURE:
                                                                                                                                                          ORGANISM: Arabidopsis thaliana
                                                                                                                                                                               TYPE: DNA
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Score 30.6;
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12;
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Length 64415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 153052, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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SEQ ID NO 153052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
                                                                                                                                                                                                                                                                               FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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NUMBER OF SEQ ID NOS: 107
                                                                                                                                         PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20
                                                                                                   NUMBER OF SEQ ID NOS: 957086
                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/261,766
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ORGANISM: Homo sapiens
                     TYPE: DNA
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Pred. No. 32;
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RESULT 6
US-09-925-065A-285326
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; ORGANISM: Homo sapiens
US-09-925-065A-285326
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Best Local Similarity 60.2%;
Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                   CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILLING DATE: 2000-10-24
                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping
TITLE OF INVENTION: Nucleotide Polymorphisms i
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICANT: Wang, David G.
TTLE OF INVENTION: Identification and Mapping of Single
TTLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                          lence 285327, Application US/09925065A:
lication No: US20040181048A1
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FILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                        433 TACCTGCACTRAAGTTAAATG 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 AACACGCACATATGTTTCCTG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 TGTGTAGAAATTTAATACATACTTCCAAACAATCCAGAGTTTTGTAGCAACTTATACTCC 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 TCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 CCTTGCCTATTCTGAACCAAGAG 86
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                                             CATION NUMBER: US 60/252,147
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Pred. No. 6.1;
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Pred. No. 9;
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in the Human Genome
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US-09-925-065A-285328
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US-09-925-065A-285327
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Best Local S
Matches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASCEEQ for Windows Version 4.0
1EQ ID NO 285327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/243,096 FILING DATE: 2000-10-24 APPLICATION NUMBER: US 60/252,147
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                                     134 AACACGCACATATGTTTCCTG 154
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433 TACCTGCACTGAAGTTAAATG
                                                                                                                         74 TCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCA 133
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Pred. No. 9;
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Pred. No. 9;
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US-09-925-065A-12385

Application US/09925065A US20040181048A1

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RESULT 10
US-11-117-187-209/c
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; ORGANISM: Arabidopsis thaliana
US-11-117-187-209
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 209, Appropriation No.
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SEQ ID NO 12385
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                                                                                                                                           Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum.
FILE REFERENCE: 108827.135
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                        ENGTH: 611587
                                            270144 TCTCTCCTGCCAAGCGAATGGATTTGTCATGCATTTGTTGCTAACTGCCGACACAAGCTG 270085
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68 GCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTC 127
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                                                                                        TCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTT 67
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                                                                                                                                         18.7%; ilarity 52.0%; Conservative
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                                                                                                                                      Score 29.4; DB 12;
Pred. No. 91;
0; Mismatches 61;
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Pred. No. 11;
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-13-30
PRIOR FILING DATE: 2001-01-16
PRIOR PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
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; ORGANISM: Homo sapiens
US-09-925-065A-805392
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                                            ; ORGANISM: Bovine US-10-750-185-47517
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                                                                                                                               APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 47517
FENCENTIAL 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47517, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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Best Local Similarity
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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                                                                                          LENGTH: 1370
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544
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  18.3%; Score 28.8;
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Pred. No. 1
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  DB 8;
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  Length 1370;
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Length 628;

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US-09-925-065A-845392
JS-09-925-065A-845392, Application US/09925065A
Sequence 845392, Application US/09925065A
Publication No. US20040181048A1
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; ORGANISM: Bovine 19866880570548
JS-10-750-623-47517
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SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 47517
LENGTH: 1370
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
CURRENT FILING DATE: 2003-12-31
                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
                                        PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/925,065A
                                                                                                                                                                                                                                                                                                                                                                                                                    PPLICANT: Wang, David G.
ITIE OF INVENTION: Identification and Mapping of Single
ITIE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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IOR FILING DATE: 2002-12-31
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HOLM, Tom
BATES, Stephen
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NUMBER: US 60/289,846
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54.8%; Pred. No. 24;
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US-09-925-065A-845392
                                                                                                                                                                                                                                                        Search completed: March 6, 2006, 10:32:51 Job time : 165.89 secs
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; ORGANISM: Homo sapiens
US-09-925-065A-33976
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Best Local
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Best Local
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56; Conserv
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DATE: 2000-11-20
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Gaps

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Title: Perfect Result No. OM nucleic -Sequence: Run on: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Searched: Scoring table: Minimum DB seq length: 0 Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: Database 0000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. score: Score 19.6 19.6 19.6 nucleic search, using sw model 30 March 5, 2006, 17:08:23; Search time 19:9642 Seconds (without alignments) 10014:946 Million cell updates/sec US-10-713-381-2_COPY_1179_1208 Query Match IDENTITY_NUC Gapop 10.0 , Gapext 1.0 4996997 seqs, 3332346308 residues 100.0 100.0 100.0 100.0 100.0 100.0 100.0 80.7 73.3 66.7 66.7 66.7 66.3 65.3 65.3 5: 6: 7: 8: 9: 110: 113: N_Geneseq_21:* 1: geneseqn198 catgcttgttcaaccgttcgtcttgttcca 30 Copyright geneseqn2003bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2003as:* geneseqn2002bs:* geneseqn2002as:* geneseqn2001bs:* geneseqn2001as:* geneseqn1990s:* geneseqn1980s:* geneseqn2004as:* geneseqn2004bs:* geneseqn2005s:* Length GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd. B AAH76335 AAH76340 AAX07408 AAX07409 AAH76332 AAH76333 ij AAH76334 ABQ75351 SUMMARIES 9993994 Aax07408 Zea mays Aax07409 Zea mays Aah76332 Z. mays M Aah76333 Z. mays M Aah76333 Z. mays M Abq75331 Human lun Abq75331 Human lun Abq75331 Human lun Abq7536 Rice stre Adj40785 Plant cDN Acl35519 Rice gene Ada72501 Rice gene Ada72530 Rice gene Description Aah76335 Z. mays Aah76340 Z. mays 一次の問題の人 3 3

ACL35067 Kice Stre	ACL35067	11	2000	62.7	18.8	. <u>4</u> .
	ADJ63835	12	1908	62.7	18.8	44
Prokary	ACA49918	8	1902	62.7	18.8	43
	AAS55583	4.	1902	62.7	18.8	42
-	ABX06821	10	1899	62.7	18.8	41
Š	ACA34769	8	1083	62.7	18.8	40
	AAS53644	4.	1083	62.7	18.8	9
Œ	ADI41918	12	883	62.7	18.8	38
Plant	ADE37244	10	883	62.7	18.8	37
Plant	ADD30938	10	883	62.7	18.8	36
Arabic	ABK65288	σ	883	62.7	18.8	35 5
_	ACN44010	11	198522	63.3	19	34
Adb32792 Human nov	ADB32792	9	5671	63.3	19	33
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	AAK90190	4	5671	63.3	19	30
/ Rice	ACL35527	H	2000	63.3	19.	29
TXOGES 8	ADE93879	10	1821	63.3	19	28
	AAC44356	ω	1388	63.3	19	27
	ADA71777	۵	1324	63.3	19	26
K1Ce	ADA73340	8	2000	64.0	19.2	25
BILL	ABQ81845	σ	349980	64.7	19.4	24
	ACD26214	9	2243	64.7	19.4	23
	AAF29956 .	4	2243	64.7	.19.4 .	22
Sequ	AAQ47668	N	2240	64.7	19.4	21
7	ADJ40977	12	2000	65.3	19.6	20
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ALIGNMENTS

AAH7633	AAH76335 DA AAH76335 standard, DNA; 30 BP.
ĕ ĕ	AAH76335;
	_29-OCT-2001 (first entry)
H X	 mays Ms45 male tissue-preferred regulatory region fragment.
×	
₹	. Ms45; male tissue; regulatory region; transcription; male rertificy;
졏	hybrid seed; ds.
×	
ž ç	Zea mays.
PN	WO200160997-A2.
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B	23-AUG-2001.
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ğq	13-FEB-2001; 2001WO-US004527.
₽ ¢	15-FEB-2000; 2000US-00504487.
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PA	(PION-) PIONEER HI-BRED INT INC.
×	The state of the state of
PH	Albertsen MC, Fox TW, Garnaat CW, Huilman G, Kendall 14;
3 🔀	2001 61/170 /66
뮸	WPI; 2001-514772/56.

Claim 5; Page 47; 50pp; English.

The invention provides a male tissue-preferred regulatory region (1) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (1) into a plant where the exogenous gene impacts male fertility of the plant and (1) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The

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A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.

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RESULT 3
AAX07408
ID AAX07408 standard; DNA; 1394 BP.
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                                                                                                                                                                                  The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences sential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays MS45 promoter fragment
                                                                                                                                                                                                                                                                                                                       A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents a DNA fragment -152 to -181 bases upstream the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
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                                                                                     l Similarity
30; Conserv
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                                                                                                             Conservative
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Pred. No. 0.0
); Mismatches
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Pred. No. 0.0045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue-preferred manner, which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding a Ms45 male tissue-preferred regulatory region - useful in mediating plant fertility, especially hybrid seed production
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                           19-JUN-1998;
                                                                                                                                                                                                                                           Ms45; male; tissue-preferred; regulatory region; plant plant tissue; differentiated; hybrid seed; fertility;
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maize; hybrid seed; fertility; ss.
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the M845 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a
                                                                                                A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                                                                         Claim 4; Page 46; 50pp;
                                                                                                                                                                                        Albertsen
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                                                                                                                                                                                                                                                                                                                                  WO200160997-A2.
                                                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                     Ms45; male tissue;

    mays Ms45 male tissue-preferred regulatory region encoding DNA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH76332;
                                                                                                                                                                                                                   (PION-)
                                                                                                                                                                                                                                                                                                                                                                                          hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH76332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 23-24; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                                                                        seed;
                                                                                                                                                                                                                   PIONEER HI-BRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGCTTGTTCAACCGTTCGTCTTGTTCCA 1208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                         2001WO-US004527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid encoding a Ms45 male tissue-preferred regulatory region mediating plant fertility, especially hybrid seed production
                                                                                                                                                                                                                                                                                                                                                                                        as.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                        Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fox TW,
                                                                                                                                                                                      W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                regulatory region; transcription; male fertility;
                                                                         English.
                                                                                                                                                                                    Garnaat CW,
                                                                                                                                                                                                                   INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garnaat CW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 2;
Pred. No. 0.007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                    Huffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huffman GA,
                                                                                                              comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1394;
                                                                                                                                                                                    Kendall
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1179

CATGCTTCTTCAACCGTTCGTCTTGTTCCA 1208

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RESULT 6
AAH76333
ID AAH7
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                                             Query Match
Best Local &
                                 Matches
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                                                                                                              The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                    A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                         Sequence 1394 BP;
                                                                                                                                                                                                                                                                            Claim 4; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-2001; 2001WO-US004527
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514772/56
                                                                                                                                                                                                                                                                                                                                                                                                   Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2000; 2000US-00504487.
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    mays Ms45 male tissue-preferred regulatory region encoding DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                 (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ms45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH76333 standard; DNA; 1394
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   Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              male tissue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                               Similarity
CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Fox TW,
                                                                                       411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory region; transcription; male fertility;
                                                           100.0%;
                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 30; DB 5; Length 1394; 100.0%; Pred. No. 0.007;
                                                                                                                                                                                                                                                                                                                                                                                                   Garnaat CW,
                               0,
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                                             Score 30;
Pred. No.
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Huffman G,
                                               0.007
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                                                         Length 1394;
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                               Indels
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                            Gaps
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lung

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RESULT 8
ABQ75351/c
ID ABQ75351 standard; cDNA; 1304 BP
XX
AC ABQ75351;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human lung specific nucleic acid
XX
KW Human; lung; lung specific nucle
XX
KW LSP; cytostatic; gene therapy; v
KW squamous cell carcinoma; gene; s
XX
OS Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays M845 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ms45; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z. mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH76334 standard; DNA; 158
                                                               Human; lung; lung specific nucleic acid; LSNA; lung specific protein; LSP; cytostatic; gene therapy; vaccine; metastasis; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 47; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514772/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2000; 2000US-00504487.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybrid seed;
                                                                                                           Human lung specific nucleic acid sequence SEQ ID NO:90.
                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleotide sequence
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                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                           26;
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                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                 CATGCTTGTTCAACCGTTCGTCTTGTTCC 29
                                                                                                                                                                                                                                                                                 CATECTTCTTCAACCGTTCGTCTTTGTTC 53
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                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      BP; 41 A; 50 C; 21 G; 46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                               ic; gene therapy; vaccine; metastasis;
carcinoma; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fox TW,
                                                                                                                                                                                                                                                                                                                                                        80.7%;
89.7%;
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                                                                                                                                                                                                                                                                                                                                          Score 24.2; D
Pred. No. 1.6;
0; Mismatches
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                                                                                                                                                                                                        ₽P
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6
                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising nucleotide sequences the MS45 gene useful for
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                                                                                                                                                                                                                                                                                                                                                                      Length 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment.
                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 9
ABZ13819
ID ABZ1
XX ABZ1
XX ARB
DT 21-J
XX ARB
DT 21-J
XX ARB
DY ARB
XX ARB
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated lung specific nucleic acid (LSNA) comprising a sequence that: (a) encodes any of the 93 amino acid comprises comprising 17 - 733 amino acids, given in ABP528673 to ABP52965; (C) (b) comprises any of 115 sequences comprising 148 - 3193 base pairs (bp), (C) given in ABQ75262 to ABQ75376; (c) selectively hybridises to (a) or (b); (C) or (d) has 60 % sequences dentity to (a) or (b). LSNA and lung specific correction (LSP) sequences have cytostatic activity and can be used in gene (c) therapy and vaccines. LSNAs and LSPs are useful for diagnosing and (c) monitoring the presence and metastases of lung cancer in a patient. An (c) continues that specifically binds to an LSP can be used for determining (c) the presence of an LSP in a sample, as well as for treating a patient the (c) lung cancer, particularly by inducing an immune response against the (c) lung cancer cell expressing the LSNAs or LSPs. In particular, these LSNAs (c) imaging and treating lung cancer (e.g. squamous cell carcinoma) and non-cyc cancerous disease states in lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-2000; 2000US-0252054P
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                              24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                  24-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana stress regulated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-2003
                                                                                                                                                                                                                                                                        WO200216655-A2.
                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                         thaliana; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                     2001WO-US026685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 22;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      gene; stress; transgenic;
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Claim 14; SEQ ID NO 31883; 1766pp; English.

isolate candidate molecules for rational drug discovery programs.

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RESULT 10
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Best Local
                                                                                                                                                 21-MAR-2001; 2001US-00815242.
06-SBF-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                      WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; ds; prokaryotic essential gene; drug design; gene.
                                                                                                                                                                                                                                                                   21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                 03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas putida.
WPI; 2003-029926/02
P-PSDB; ABU40143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prokaryotic essential gene #25670.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACA44013 standard; DNA; 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress regionse. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                    (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1542 BP; 345 A; 382 C; 370 G; 445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying a stress condition to which a cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 144; SEQ ID NO 1624; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying a stress c producing plants with
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                  ELITRA PHARM
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Trawick JD,
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Carr (
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Pred. No. 91;
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                                                  Haselbeck R, Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          cell proliferation;
                                                  Ohlsen
Forsyth
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Xu HH;
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The invention relates to an isolated nucleic acid comprising any one of CC the 6213 antisense sequences given in the specification where expression CC of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid CC encoding a polypeptide whose expression is inhibited by the antisense cCC nucleic acid; (2) a host cell containing the vector; (3) an isolated CC encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding CC polypeptide (3) producing the polypeptide; (6) inhibiting cellular cC proliferation, (7) identifying a compound that influences the activity of agene in an operon required for proliferation, (7) identifying a compound that influences the activity of containing the vector of the product or that has an activity against a biological pathway confidentifying a gene required for cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiocit; (10) profiling a compound that inhibits of the gene product is overexpressed or underexpressed; (12) determining the extent compound to a compound that inhibits of the gene product is overexpressed or underexpressed; (12) determining the extent contains; or (13) identifying the target of a compound that inhibits the contains; or (13) identifying the target of a compound that inhibits the containing or an organism. The antisense nucleic acids are useful for contentifying proteins or screening for homologous nucleic acids required condentifying proteins or for screening homologous nucleic acids required condentify and discovery programs. Or for screening homologous nucleic acids are useful condentify the condents or for a condentify the condent or homologous nucleic acids.
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Sequence 2397 BP; 415 A; 825 C; 781 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                          drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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RESULT 11 ACL37526 822228 밁 Ś Matches Query Match 22-JUN-2001; 2001US-0300112P. 24-AUG-2001; 2001US-0314662P. 26-SEP-2001; 2001US-0325277P. 21-NOV-2001; 2001US-0332132P. 30-JAN-2003 21-JUN-2002; 2002WO-US019668 Oryza sativa. ss; abjotic stress tolerance; transgenic plant; plant; cereal; WO2003008540-A2 Rice stress-regulated promoter SEQ ID NO:16089. 02-JUN-2005 ACL37526; ACL37526 standard; cDNA; Local 516 CATGCTGGTACAACCGTTCGGCTTG 540 1 CATGCTTGTTCAACCGTTCGTCTTG 25 22; Similarity 88.(22; Conservative (first entry) 67.3%; 2000 <u>.</u>; Score 20.2; D Pred. No. 1.2e 0; Mismatches В₽ 2e+02; BG 8 3; Indels Length 2397; 0; Gaps

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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to

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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the stress, osmotic stress or any of their combinations. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2000 BP; 607
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                       WPI;
                                                                                                             22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0332277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                           agriculture
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                                                                                                                                                                                                    30-JAN-2003
                                                                                                                                                                                                                             WO2003008540-A2
                                                                                                                                                                                                                                                                                                                 Rice stress-regulated promoter SEQ ID NO:13539.
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                                                                                    (SYGN)
                                                                                                                                                                                                                                                                                          abiotic stress tolerance; transgenic plant; plant; cereal;
                       2003-248011/24
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                                                                                    SYNGENTA PARTICIPATIONS
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T, Provart
                                              Briggs SP,
T, Provart
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                                                                                                                                                                                                                                                                                                                                          entry)
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N, Ricke
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                                               Cooper B, G
N, Ricke D,
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Pred. No. 1.4e+02;
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                                                Glazebrook J,
D, Zhu T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an abiotic stress such as cold
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New

stress-responsive nucleic acid, useful for altering

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Glazebrook

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RESULT 13
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ID ADJ40785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant; nutrition; apical dominance; dwarfism; early flowering; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stress, osmotic stress or any or their communation is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       responsiveness of a plant, e.g. cereal, stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADJ40785
                                                                                                                                                               (BRIG/)
(COOP/)
(GLAZ/)
(GOFF/)
(KATA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2004016025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant cDNA #1785
                                                                                                                                                                                                                                                                                                   (MOUG/)
                                                                                                                                                                                                                                                                                                                                                                                        04-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota
                                                                                                       (PROV/)
                                                                                                                                         KREP/)
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                                    JEPS J.
PROVART N.
RICKE D.
ZHU T.
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                                                                                                                                                                                                                                           BRIGGS S P. COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                   BUDWORTH P. MOUGHAMER T.
                                                                                                                                                                  GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                     GLAZEBROOK J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; cDNA; 2000 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000 BP; 552 A; 438 C; 444 G;
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                                                                                                                                                                                                                                                                                                                                                                                                              2001US-0325277P.
2001US-0325448P.
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                                                                                                                                                                                                                                                                                                                                                                                        2002US-0370620P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4e+02;
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RESULT 14
ACL35519
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CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

CC or constitutive transcription of an operatively linked nucleic acid

CC segment. The invention also relates to a method for augmenting a plant

CC genome and a method of identifying a gene, where its expression is

cc antered in the seed, leaf, stem, panicle, pollen, root or is constitutive

CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,

CC canola, cotton, peanut, tobacco or sugar best, preferably maize, barley,

CC sorghum, rice or wheat. The polymuclectides and the polypeptides they

CC sorghum, rice or wheat the polymuclectides and the polypeptides they

CC encode are useful for manipulating crop plants to alter or improve

CC proteins, to incur resistance to insecticides, viruses or fungi, and to

CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants

CC early flowering or altered metabolic pathways. This sequence are represents a

CC plant nucleic acid of the invention. Note: The sequence data for this

CC plant nucleic acid of the invention are the sequence data for this

CC plant nucleic acid of the invention are the sequence data for this

CC plant nucleic acid of the printed specification but was obtained in

CC electronic format directly from USPTO at sequence has powers.
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Best Local S
Matches 23
                                                                                              22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
  Moughamer
                                                                                                                                                                                                21-JUN-2002; 2002WO-US019668.
                                                                                                                                                                                                                                                                                       WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                      agriculture
                                                                                                                                                                                                                                                                                                                                                                                      ss; abiotic
                                                                                                                                                                                                                                                                                                                                                                                                                        Rice stress-regulated promoter SEQ ID NO:14082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2005
                                                        (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2000 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26; SEQ ID NO 1785; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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Briggs SP,
T, Provart
                                                                                                                                                                                                                                                                                                                                                                             stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.7%;
ilarity 82.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA; 1735
Cooper B,
N, Ricke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20; DB 12;
Pred. No. 1.4e+02
0; Mismatches
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                Glazebrook J,
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              Katagiri
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New stress-responsive nucleic acid, useful for altering the responsiveness of a plant, e.g. cereal, to an abiotic stress such stress, salt stress or osmotic stress.
                                                                                                                     as
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Claim 48; SEQ ID NO 14082; 89pp; English.

22 and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polypucleotides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polypucleotides. Also disclosed are reethods for using the polypucleotides and polypeptides to alter the responsiveness of a plant to abjoict extress. The invention is useful in 22 agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abjoict extress condition. It is also useful for selecting an agent that alters abjoict stress regulated 22 polypucleotide expression in a plant cell, and to identify a homolog or ortholog to an abjoict extress responsive polypucleotide. The nucleic acid 22 molecule and the polypeptide encoded by it are useful in altering the molecule and the polypeptide encoded by it are such as cold stress, salt stress, osmotic stress or any of their combinations. The present sequence of is used in the exemplification of their nombinations. a homolog or he nucleic acid sequence

Sequence 1735 BP; 502 A; 368 C; 279 G; 581 T; 0 U; 5 Other;

Ś Query Match Matches v 22; Similarity CTTGTTCAACCGTTCGTCTTGTTCCA 30 65.3%; ilarity 84.6%; Conservative ٥, Score 19.6; DB 11; Pred. No. 2e+02; 0; Mismatches 4; Indels Length 1735; ٥, Gaps

RESULT 15 ADA72061 ADA72061 standard; 394 CATGITTAACCGITCGICTTATICAA 419 DNA; 2000 ₽P

문

gene; Plant; bacterial infection; fungal infection; viral infection; rice; Rice gene, SEQ ID 5386. 20-NOV-2003 ADA72061; ds. (first entry)

Oryza sativa

WC2003000898-A1

03-JAN-2003.

22-JUN-2001; 2001WO-IB001105.

22-JUN-2001; 2001WO-IB001105

(SYGN) SYNGENTA PARTICIPATIONS Ą

Chang H, C Katagiri F, Chen W, F, Quan Cooper B, S, Tao Y, S Glazebrook J, (Whitham S, Xie Goff SA, T, Hou zou ç,

WPI; 2003-248011/24

Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression. ה ל ס

27; SEQ ID NO 5386; 899pp; English

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered ä

the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

Sequence 2000 BP; 605 A; 377 C; 326 G; 690 T; 0 U; 2 Other;

Query Match 65.3%; Score 19.6; DB 8; Length 20 Best Local Similarity 84.6%; Pred. No. 2.1e+02; Matches 22; Conservative 0; Mismatches 4; Indels 5 CTTGTTCAACCGTTCGTCTTGTTCCA 30 Length 2000; 0; Gaps

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974 CATGITTAACCGITCGICTTATICAA 999

Search completed: March 5, 2006, 18:11:42 Job time: 19.9642 Becs

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No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST: *
1: 9b
2: 9b
3: 9f
4: 9f
5: 9
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Match Length DB
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Gapop 10.0 , Gapext 1.0
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gb_est2:*
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10 CG224225
9 CC656933
10 CW445575
10 CG700474
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BU0300139
CN137013
AA811551
CR0642759
CR064270
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CC848693
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CC656939 OGMDQ20TV
CC656933 OGMDQ2OTV
CC656933 OGMDQ2OTM
CCW445575 fsbb001f1
CG700474 ZMMB601f1
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CG13701 OX1 54 E0
CR137013 OX1 54 E0
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CR12459 Reverse s
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CR1233964 Reverse s
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CR126169 NDL.2114.
CC860012 NDL.2113.
CC853973 LM SH5 OC
R12618 Yf57508 F1
R12618 Yf57508 F1
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67.3	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	
431	1205	967	836	807	779	899	639	615	603	602	600	598	590	560	559	536	515	514	398	396	373	353	
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R32995	B10570	BZ684538	BH480110	CD836362	CD825116	AQ260121	CV153844	AQ453944	BZ694195	CL583422	BH876120	CW788317	CV153842	CA230882	AV825937	AV439701	BP561510	BG354154	BP836596	BE522930	BP857382	AQ261553	
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R32995 yh73g09.rl	B10570 T15J6-T7 TA	BZ684538 PUBGO31TD					4	_		CL583422 OB Ba00	BH876120 hr29b04.g	CW788317 SP Ba004	CV153842 Eucinetus				_						

ALIGNMENTS

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Query Match Best Local Matches 3	FEATURES SOURCE	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 CC656939/c LOCUS DEFINITION ACCESSION VERSION
Match 100.0%; Score 30; DB 9; Length 687; Local Similarity 100.0%; Pred. No. 0.024; les 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelawatigr.org Seq primer: TF Class: methylation filtered. Location/Qualifiers 1. 687 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db xref="eaxon:45717" /clone="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"	a; Viridiplantae; Streptophyt; phyta; Magnoliophyta; Liliops; anicoideae, Andropogoneae; Zea anicoideae, Andropogoneae; Zea , C. A. Ger, Budiman, M. A. A., Fraser, C. M., Budiman, M. A. W., Nuberg, A., Robbins, D. an um for Maize Genomics hed (2002) Sss. COWDQ2OTM Cathy Whitelaw	CC656939 687 bp DNA linear GSS 19-JUN-2003 OGWDD20TV ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0554D15, genomic survey sequence. CC656939 CC656939.1 GI:32060231 GSS. Zea mays Zea mays

1 CATGCTTGTTCAACCGTTCGTCTTGTTCCA 30

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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Whitelaw,C.A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG1AG08TH
Contact: Cathy Whitelaw
              1 (bases 1 to 963)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
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CG224225.1 GI:34124113
Unpublished Other GSSs:
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Fax: 301-838-0208
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llarity 100.0%;
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/clone=1bb="ZM 0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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Lone ZMMBMa0554D15
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4041 Forest Park Ave, 5
Tel: 314 615 6979
Fax: 314 615 5975
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                                                                                                                                                                                                                                                            Email: jbedell@oriongenomics.com
Plate: fsbb001f170 row: m colu
Seq primer: k Reverse
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Sorghum bicolor
Sorghum bicolor
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 296)
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Class: methylation filtered.
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Email: whitelaw@tigr.org
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9712 Medical Center Drive,
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                                                                                                                                                                                                  High quality sequence stop: 296.
Location/Qualifiers
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                                                                                                                                                                                                                                              Class: methylation filtered
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/clone=1b="ZM 0.7 1.5 KB"
/note="Vector: pBCSK ; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
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/mol_type="genomic DNA"
/strain="B73"
                                                                                                                   /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
                                           /clone_lib="Sorghum methylation filtered library (LibID:
104)"
                                                                                /db_xref="taxon:4558"
/clone="fsbb001f170m16"
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Matches 24
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Clone QHJ7N19, mRNA seque
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EST.
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Zea mays genomic clone
5', genomic survey sequence.
CG700474

CG700474

CG700474.1 GI:37688275

GSS.
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Class: BAC ends
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Zohovetz,V.,
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Sequencing of the maize genome
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Pel: 732 445 3801
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/clone="ZwMBBc0174H15"
/lab_host="E. coli_DH10B"
/clone_lib="ZwMBBc (EcoRI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young,S., Kavchok,S., Keizer,G., Bronzino, Fuks,G., Yu,Y., Wing,R. and Messing,J. the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                74.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      @waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91.3%;
                                                                                534 bp mRNA linear QH_EFGHJ sunflower RHA280 Helianthus mRNA sequence.
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Pred. No. 60;
0; Mismatches
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Pred. No. 0.3;
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                                                                                                                      EST 23-AUG-2002
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Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                   Helianthus annuus
Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; Campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
                                                                                                                                                                                                                                               BU030489 626 bp mRNA linear E
QHJ15120.yg.abl QH EFGHJ sunflower RHA280 Helianthus
clone QHJ15120, mRNA sequence.
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                                                                                                                                                                         Helianthus annuus (common sunflower)
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Helianthus annuus
Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteroide; Campanulide; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3046, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: akozik@atgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heliantheae; Helian
1 (bases 1 to 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 1-(530)-742-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCTTGTTCAACCGTTCGTCTTGTT 27
(bases 1 to 626)
.ik.A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
.h. van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  details.
te: QHJ7 row: N column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Separate CDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size blas. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_IJB=0H_EGHJ_eunflowers_RNA280
TAG_SEQ=CGAATGCGGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:4232"
clone="QHJ7N19"
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(mol_type="mRNA"

/cultivar="RHA280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone lib="QH_EFGHJ sunflower RHA280"
note="Vector: pBRcDNASfiAB; The library was constructed
rom 11 different sources of RNA from a single genotype.
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88.5%;
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Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CN137013 792 bp mRNA linear EST 01-APR-20031_54_E01.g1_A002 Oxidatively-stressed leaves and roots Sorghum bicolor cDNA clone OX1_54_E01_A002 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3046, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                  Other_ESTs: OX1_54_E01.b1_A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: QHJ15 row: I column:
Location/Qualifiers
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Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                          Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R.R., Liang,C., Sun,F., Sullivan,R., Lim,S., Eastman,A. and Pratt,L.H.
An EST database from Sorghum: oxidatively stressed leaves and roots
                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://compgenomics.ucdavis.edu,
                                                                                                                                                                                                       Unpublished (2003)
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mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Separate CDNAs were generated using primers that incorporated unique 5, and 3, tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_TISSUE=flowers environmental stress
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/note="Vector: pBRcDNASfiAB; The library was constructed
from 11 different sources of RNA from a single genotype.
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/mol_type="mRNA"
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/clone="QHJ15I20"
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SEQ=CGAATGCGGG"
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Pred. No. 1.9e+02;
0; Mismatches 3;
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Trace considered overall poor quality

www-bio.llnl.gov/bbrp/image/image.html

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AA811551/c
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AA811551.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science, plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA811551 154 bp mRNA linear EST 19-FEB-1998 oa99e03.81 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320412 3' similar to SW:COPE_BOVIN 028104 COATOMER EPSILON SUBUNIT ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: Sug5 (CTTCTGCTCTAAAAGCTGCG).
                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 154)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exclude polyA.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                             Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/clone="OX1 54 E01 A002"
/lab host="DH10B-TI phage-resistant E. coli"
/lab host="DH10B-TI phage-resistant E. coli"
/clone_llb="Oxidatively-stressed leaves and roots"
/clone_llb="Oxidatively etressed, Vector: pME18S-F13; Site 1:
/note="Organ: Leaf and Root; Vector Root and Poole And Root and Poole And Root and Poole And Root and
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/cultivar="BTx623"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.7%;
88.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:2881162
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                          David Allman,
                                                                                                                                                                                                                    M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
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REFERENCE
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CR192459/c
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Best Local S
Matches 24
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JOURNAL
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                               307
                                                             N
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                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                           CR192459.1 GI:49971308
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR192459 351 bp DNA Reverse strand read from insert in 5'HPR chromosome engineering clone MHPN146a06, CR192459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                                                                                                                                                                                                                                                                              Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 1232 Std Error:
Seq primer: -40ml3 fwd. ET from A
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR192459
                                                                                                                                                                                                                                                                                                                                            Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G.,
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Schurrognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                          Similarity
                                                    ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
                            ATGCTGGTCCAGCCGTTCGTGATGTTCCA 279
                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 351)
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                      /organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN146a06"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             went through one round of na
constructed by Bento Soares

    Double-stranded cDNA was ligated to Sco RI adaptors.
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified py773 vector. Library
went through one round of normalization, and was

                                                                                                                                                                                                                                                                                                                               and Bradley, A.
                                                                                                                                                                                                                                                                     ocation/Qualifiers
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'mol_type="mRNA"
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                                                                                                      70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                         Score 21; DB 11;
Pred. No. 2.1e+02;
0; Mismatches 5
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Pred. No. 1.8e+02;
0; Mismatches 5;
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5'HPRT insertion targeting and
46a06, genomic survey sequence.
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                                                                                                                       Length 351;
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Nishijima,I., Yu,Y.,
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                                                                                       Gaps
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2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30

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ACCESSION
VERSION
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VERSION
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CR233964/c
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source
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AUTHORS
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ORGANISM
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CR064270/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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Best Local :
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; But
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi, Muroidaa; Muridae; Murinae; Mus.
1 (bases 1 to 599)
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR064270.1 GI:49797742
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rogers,J. and Bra
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
Rogers,J. and Bradley,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence; MICER. Mus musculus (house mouse)
Mus musculus
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           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                   /organism="Mus musculus"
/mol type="genomic DWA"
/db xref="taxon:10090"
/clone="MHPN144108"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN190119"
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0;
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Pred. No. 2.2e+02;
0; Mismatches 5
                                         Score 21; DB 11;
Pred. No. 2.3e+02
           Mismatches
                                     2.3e+02;
                                                                    Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 571;
   Indels
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Nishijima,I., Yu,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 06-JUL-2004
targeting and
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               832 bp DNA linear GSS
NDL.2I14.T7 Notre Dame Liverpool Aedes aegypti genomic
NotreDame Liverpool-2I14, genomic survey sequence.
CC848693
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                                                                                                                                                                                                                                                        Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.

1 (bases 1 to 832)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
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l Similarity 82.8%;
24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR188179 769 bp DNA linear GSS 06-JUL-2004 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN234h03, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
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CR188179.1 GI:49967028
                                     Seq primer: T7
Class: BAC ends.
                                                              Email: enta@tigr.org
Library was provided
Seq primer: T7
                                                                                                                                                                                                                     Other_GSSs: NDL.2I14.SP6
Contact: Brendan Loftus
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                                                                                                                                                           9712 Medical Center Drive,
                                                                                                                                                                                                    Department of Eukaryotic Genomics
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                                                                                                                      Fax: 301-838-0208
                                                                                                                                      Tel: 301-838-3543
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MHPN234h03"
/clone_lib="MHPN"
    Location/Qualifiers
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Pred. No. 2.3e+02;
0; Mismatches 5
                                                                              David Severson
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Search completed: March Job time: 141.632 secs

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CC860012/c
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242 ATCCTTGTTCAACCATTTGTCTTGATTCA
                                                                                                                                                                                                                                                                                                                                                                                      Email: enta@tigr.org
Library was provided l
Seq primer: T7
Class: BAC ends.
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1 (bases 1 to 835)

Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti
Unpublished (2003)
                                    N
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Tel: 301-838-3543
Fax: 301-838-0208
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Contact: Brendan Loftus
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                                    ATGCTTGTTCAACCGTTCGTCTTGTTCCA
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                                                                        Conservative
                                                                                                                                                            /clone="NotreDame Liverpool-2113"
/clone lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched Li larvae by David Severson at the University of Notre Dame and Hongbin Zhang"
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/db xref="taxon:7159"
/clone="NotreDame Liverpool"
/clone lib="Notre Dame Liverpool"
/clone lib="Notre Dame Liverpool"
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                                                                                                                                                                                                                                                                           /organism="Aedes aegypti"
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3ndopterygota; Diptera; Nematocera; Culicoidea;
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0; Mismatches
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Pred. No. 2.4e+02
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                                                                        Mismatches
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Maximum DB seq length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
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_6/ptodata/1/ina/RE_COMB.seq:*
_6/ptodata/1/ina/backfiles1.seq:*
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  US-08-880-499-1
US-07-937-609-15
US-07-937-609-15
US-08-029-170-15
US-09-949-016-16262
US-09-949-016-1438
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US-09-921-992-3
US-09-921-932-3
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US-09-921-932-3
US-09-921-932-3
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Sequence 2, Appli
Sequence 15, Appl
Sequence 15, Appl
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58.0	58.0	58.0	58.0	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3
789	719	601	331	276237	265038	183202	141115	72843	40505	9472	8074	8073	2009	999	978	601	601	601	499	499
ω	w	w	w	w	w	w	w	ω	ω	N	w	ω	N	w	w	ω	w	w	w	ω
US-09-252-991A-11034	US-09-107-433-820	US-09-949-016-178197	US-09-640-211A-169	US-09-949-016-17504	US-09-949-016-15779	US-09-949-016-13614	US-09-949-016-17490	US-09-949-016-12574	US-09-949-016-13439	US-08-325-547-9	US-09-949-016-16645	US-09-949-016-12327	US-07-958-222A-1	US-08-961-527-193	US-08-858-207A-174	US-09-949-016-204030	US-09-949-016-204029	US-09-949-016-142937	US-09-270-767-17275	US-09-270-767-1993
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
11034, A	820; App	178197,	169, App	17504, A	15779, A	13614, A	17490, A	12574, A	13439, A	9, Appli	16645, A	12327, A	1, Appli	193, App	174, App	204030,	204029,	142937,	17275, A	1993, Ap

ALIGNMENTS

Application US/08880499 6037523

; MOLECULE TYPE: DNA (genomic)
; TOPOLOGY: linear
; STRANDEDNESS: single.
n
1: 1394
Ω
; TELEPHONE: (515) 248-4800
2
, REFERENCE/DOCKET NUMBER: 0578
; NAME: Sweeney, Patricia A.
; ATTORNEY/AGENT INFORMATION:
; CLASSIFICATION: 800
; FILING DATE: CONCURRENTLY HEREWITH
Z
; CURRENT APPLICATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.30
SYSTEM:
₩
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; ZIP: 50131
; COUNTRY: USA
; STATE: Iowa
; CITY: Johnston
; CORRESPONDENCE ADDRESS:
2
OF INVENTION: AND METHOD OF USING SAME
INVENTION: MALE
: Kendall,
: Huffman, Gary
: Carl
Fox, Tim W.
APPLICANT: Albertson, Marc C.
GDNDAGE INTOXIDATION:

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Query Match

100.0%; Score 30;

DB 3; Length 1394;

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RESULT 3
US-07-937-609-15
; Sequence 15, Application US/07937609
; Patent No. 5319073
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US-08-880-499-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1394 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                               Query Match
         GENERAL INFORMATION:
APPLICANT: WANK, Stephen A.
APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
OBJORNES US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
CLASSIFICATION: 800
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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STREET:
CITY: J
                                                                                                                                                                                                                                                                                                             Local Similarity
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ZIP: 50131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC. STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O STREET: Box 1000
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Pred. No. 0.0012;
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; Mismatches 0;
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US-08-029-170-15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2243 hass
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Best Local Similarity
Matches 23; Conserv
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FILING DATE: 07-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/861,769
FILING DATE: 01-APR-1992
PRIOR APPLICATION OLATA:
APPLICATION NUMBER: US 07/928,033
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/166 NIHD
TELEPHAN: (703)836-9300
TELEPHAN: (703)836-9300
                                                                                                                                                                                                                                             Sequence 15, Application US/08029170 Patent No. 6169173
                                                                                                                                                                                                             APPLICANT: WANK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/937,609
APPLICATION NUMBER: US/07/937,609
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MOLECULE TYPE:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: US 07/831,248
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                       APPLICANT: WANK, Stephen A.
TITLE OF INVENTION: CLONING AND FUNCTIONAL EXPRESSION OF
TITLE OF INVENTION: CHOLECYSTOKININ RECEPTOR-ENCODING DNA
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
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CITY: Alexandria
                                                                      CITY: Alexandria
STATE: VA
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                                                                                                      STREET:
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                                                                                                        ADDRESSEE: Foley & Lardner Suite 500 STREET: 1800 Diagonal Road, Suite 500
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1800 Diagonal Road, Suite 500
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79.3%;
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Pred. No. 55;
0; Mismatches
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; NAME/KEY:
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US-08-029-170-15
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Best Local Similarity
Matches 23; Conserv
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NERAL INFORMATION:
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PRIOR APPLICATION DATA:
US 07/937,609
                                            ZIP: 22313-0299

READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        DRESSEE:
                                                                                                                                                                                   SPONDENCE ADDRESS
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CE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                 Application US/09443745
                                                                                                                                                     1800 Diagonal Road, Suite 500
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ION NUMBER: US 07/861,769
ATE: 01-APR-1992
                                                                                                                  USA
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CATION DATA:
US 07/831,248
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136..1494
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ATION DATA:
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YSTEM: PC-DOS/MS-DOS
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               DATA:
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79.3%;
                              Release #1.0, Version #1.25
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      US/09/443,745
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Pred. No. 55
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; LOCATION: 136
US-09-443-745-15
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Best Local Simi
Matches 23;
 Query Match
                           ORGANISM: Human
-09-949-016-16262
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SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERICE/DOCKET NUMBER: 4
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US 07/831,248
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ON NUMBER: US 07/861,769
TE: 01-APR-1992
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                                                                                                                                                                                                                                                                                                                    Application US/09949016
                                                                                                                                                                                                                     ON NUMBER: US/09/949,016
                                                                                             for Windows Version 4.0
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MBER: US 07/937,609
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                                                                                                                                                                                                                                             Craig et al.
OLYMORPHISMS IN KNOWN
WITH HUMAN DISEASE, MI
                                                                                                                                                                                                        2000-04-
 63.3%; Score 19;
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                                                                                                                                                                                                                                                 METHODS
 DB 3;
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Length 45571;
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OF DETECTION AND USES THEREOF
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US-09-949-016-1438/c
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                                     US-09-949-016-1438
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1438, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
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Matches
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Query Match
                                                                                                           SEQ ID NO 1438
                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 101918-200 (OCR-941)
CURRENT APPLICATION NUMBER: US/09/368,590
CURRENT FILING DATE: 1999-08-04
EARLIER APPLICATION NUMBER: 60/095,657
EARLIER FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 8
NOTTARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR TITLE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Solimena, Michele
                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                    LENGTH: 8756
TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: (2266)...(2268)
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LOCATION: (1021)...(1023)
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LOCATION: (1)...(6879)
NAME/KEY: unsure
LOCATION: (100)...(102)
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 Score 18.8;
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Pred. No. 1
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1.3e+02;
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OF DETECTION AND USES THEREOF
Length 8756;
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US-09-949-016-13180/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-961-527-132
                                                                                                                                                                                                                                                                                             Sequence 13180, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION APPLICATION:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TOPPOSITE OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 23; Conserv
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE.
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TYPE: nucleic acid
STRANDEDNESS: double
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0; Mismatches 7;
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RIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS:

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; ORGANISM: Drosophila melanogaster US-09-270-767-29480
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; LOCATION: (1)...(112874)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13180
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                                                                                                                                           SEQ ID NO 13492
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SEQ ID NO 29480
                                                                                                                                                                                                                                                                                                              Sequence 13492
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                                                                       ORGANISM: Drosophila melanogaster
                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
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                     Local
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E OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster REFERENCE: File Reference: 7326-094
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                                                                                                                                                                                                                                                                              INFORMATION:
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       21; Conservative
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l Similarity 76.7%;
23; Conservative
                     Similarity
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21; Conservative
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                 62.0%;
Score 18.6; DI
Pred. No. 1.1e
0; Mismatches
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Pred. No. 2e+02;
0; Mismatches 7; Indels 0;
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Pred. No. 9
                 .1e+02;
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US-09-573-080A-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 7, Application US/09573080A
Patent No. 6828097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY: repeat region
LOCATION: (1)..(2710)
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: JOAN, KNULL ROGAN, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/096,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/248,796A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Keith Weinstock et al
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
ITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
ILE REFERENCE: 107196.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 TGCTTGTTGAAGAGTTCTTCTTGTT 199
                                                                                                                                                                                CATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE: 30307
IT APPLICATION NUMBER: US/0:
IT FILING DATE: 2000-05-16
OF SEQ ID NOS: 479
                                                                                                                                                                                                                   XEY: misc_feature
INFORMATION: n i
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                                    ACCESSION NUMBER: Database for repetitive elements (repbase)
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                                                                                                                             of Molecular
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78.6%;
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Pred. No. 1.4e+02;
0; Mismatches 6;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,488
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2070-10-03
PRIOR PILING DATE: 2070-10-03
PRIOR FILING DATE: 2070-10-03
PRIOR SEQ ID NOS: 207012
SEQ ID NO 200252
LENGTH: 601
TYPE: DNA
J. ORGANISM: Human
US-09-949-016-200252
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US-09-949-016-200252/c
; Sequence 200252, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
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Search completed: March Job time : 8.38752 secs
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                                                                                                                                                                                                    Query Match 60.0%; Score 18; DB 3; Length 601; Best Local Similarity 80.8%; Pred. No. 1.8e+02; Matches 21; Conservative 0; Mismatches 5; Indels
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Match Length
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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              US-09-925-065A-863989

4 US-09-925-065A-546217

8 US-10-425-115-100318

7 US-10-425-563-5

9 US-10-972-789A-5
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8 US-10-741-600-1767-6

3 US-09-938-842A-1624

3 US-09-938-842A-1624

7 US-10-282-122A-31883

7 US-10-282-122A-31883

7 US-10-238-1785

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10S-10-243-745-15

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Sequence 4, Appli
Sequence 1, Appli
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Sequence 2, Appli
Sequence 3, Appli
Sequence 90, Appl
Sequence 17676, Ap
Sequence 17674, Ap
Sequence 1624, Ap
Sequence 1785, Ap
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Sequence 2544, Ap
Sequence 1977, Ap
Sequence 5, Appli
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US-10-369-493-33483	US-10-260-238-2535	US-10-282-122A-37788	US-09-815-242-9220	US-10-472-928-2217	US-10-437-963-40048	US-10-335-977-2195	US-10-335-977-2194 '	US-10-282-122A-22639	US-09-815-242-7281	US-10-225-066A-971	US-10-225-068-183	US-10-374-780A-381	US-10-225-066A-971	US-10-225-068-183	US-09-934-455-279	US-09-925-065A-953397	US-09-925-065A-936360	US-09-925-065A-936359	US-09-925-065A-472473	US-10-087-192-244	US-09-764-872-729	
	Sequence 2	Sequence 3	Sequence 9	Sequence 2	Sequence 4	Sequence 2		Sequence 2	Sequence 7	Sequence 9	Sequence 1	Sequence 3	Sequence 9	Sequence 1	Sequence 2	Sequence 9	Sequence, s	Sequence 5	Sequence 4	Sequence 2	Sequence 7	
ū	2535, Ap	37788, A	9220, Ap	2217, Ap	40048, A	2195, Ap	•	22639, Ā	۳	971, App	-	•	•	•	279, App	953397,	936360,	936359,	47	244, App	729, App	

ALIGNMENTS

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RESULT 2
US-10-713-381-9
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Best Local S
Matches 30
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PRIOR FILING DATE: 1997-06-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/713,381 FILING DATE: 2003-11-14
INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                          Application US/10713381
No. US20040221331A1
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                                   ALBERTSEN, MARC C.
FOX, TIMOTHY W.
GARNAAT, CARL W.
HUFFMAN, GARY
KENDALL, TIMMY L.
                                                                                                                                                                                                                                                                                                                      100.0%; Score 30; DB 8;
llarity 100.0%; Pred. No. 0.008;
Conservative 0; Mismatches 0
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FILE REFERENCE: 578R

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CURRENT APPLICATION NUMBER: US/10/713,381; CURRENT FILING DATE: 2003-11-14; PRIOR APPLICATION NUMBER: 08/880,499; PRIOR FILING DATE: 1997-06-23; NUMBER OF SEQ ID NOS: 24; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 9; LENGTH: 255
TYPE: DNA; ORGANISM: Zea mays
US-10-713-381-9
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Best Local Similarity
                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10713381 Publication No. US20040221331A1
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Publication No. US20040221331A1
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APPLICANT: GARMAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT APPLICATION NUMBER: US/880,499
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOYHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
                                                                                                                                                                                                                  APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                  1179 CATGCTTCTTCAACCGTTCGTCTTGTTCCA 1208
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100.0%; Pred. No. 0.013;
ative 0; Mismatches 0
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Pred. No. 0.011;
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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2:
; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DMA
; ORGANISM: Zea mays
US-10-713-381-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                   Sequence 90, Application US/10001857
Publication No. US20020183500A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/10713381 Publication No. US20040221331A1
              SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
LENGTH: 1304
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                    TITLE OF INVENTION: Compositions and Methods Relating FILE REFERENCE: DEX-0273 CURRENT APPLICATION NUMBER: US/10/001,857 CURRENT FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/252,054 PRIOR FILING DATE: 2000-11-20 NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                    APPLICANT: Macina, Roberto APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 158
TYPE: DNA
ORGANISM: Zea mays
ORGANISM: Homo sapien
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26; Conserv
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Sun, Yongming
Liu, Chenghua
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Chen, Sei-Yu
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Pred. No. 2.8;
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Pred. No. 0.013;
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US-10-001-857-90

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                                                                             Best Loc
Matches
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                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17676, Application US/10741600 Publication No. US20050026169A1
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                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(198090)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables
                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                  OFTWARE: Fast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (1)...(1980090)
OTHER INFORMATION: n = A,T,C or G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             ENGTH: 1980090
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1948918 ATTCTTGCTGAACAGTTCGTCTTGTACCA 1948890
                                                                                                                                                                                                                                                                                                                                                                                                                        LICANT: CARGILL, Michele et al. —
LE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
LE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ence 6815, Application US/10719993 ication No. US20040265849A1
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                                    2 ATGCTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                 Similarity
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                                                                               Conservative
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                                                                                            70.0%;
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                                                                      Score 21; DB 8; Len; Pred. No. 2.2e+02; Migmatches 5;
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Pred. No. 2.2e+02;
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                                                                                            Matches
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; ORGANISM: Arabidopsis thaliana US-09-938-842A-1624
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US-09-938-842A-1624
                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                 SEQ ID NO 1624
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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PRIOR PILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu Tong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELICANT: Zhu, Tong
TILE OF INVENTION: STREESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TILE OF INVENTION: SAME; AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TILE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1542
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                                                                                                                  Local Similarity
237 CATGATTGTTCAACCAATCGTCGGTTTCCA 266
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                                           TGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                             68.0%;
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80.0%; Pred. No. 1.
                                                                                                             Pred. No. 1
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                                                                                       Mismatches
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                                                                                                                                     DB 3;
                                                                                                                                   Length 1542;
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-282-122A-31883
                                                                                                                                                                                                         US-10-260-238-1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                         Sequence 1785, Application US/10260238 Publication No. US20040016025A1 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
                                                         APPLICANT: Budworth, Paul R.
APPLICANT: Woughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                             516
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Zamudio, cuz
Zamudio, cuz
Tone, Cheryl
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Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck,
Goff, Stephen A.
Katagiri, Fumiyaki
                                        Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           67.3%;
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                                                                                                                                                                                                                                                                                                                                                                            0;
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; TYPE: DNA; Oryza sativa; ORGANISM: Oryza sativa US-10-260-238-1785
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US-10-437-963-96639/c
                                                                                                                RESULT 14
US-10-425-115-3534/c
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CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR APPLICATION NUMBER: US 60/370,620
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LENGTH: 2000
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Best Local Similarity
                                                     Sequence 3534, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 96639
LENGTH: 640
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                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 6077
APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT4530_94716C
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                CTTGTTCAACCGTTCGTCTTGTTCCA 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Provart, Nicholas
Ricke, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boukharov, Andrey A.
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82.1%;
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Pred. No. 2.9e+02;
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Pred. No. 2.3e+02;
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CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 3534
LENGTH: 901
TYPE: DNA
ORGANISM: Zea may8
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_103225C.1
US-10-425-115-3534
                                                                             ġ
Search completed: March 6, 2006, 03:55:17 Job time: 45.1372 secs
                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-260-238-1977
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Best Local Similarity 84.6%;
Matches 22; Conservative
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
                                                                                                                                                                                                                                                                                         Q ID NO 1977
LENGTH: 2000
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                                                                                                                                                                                                                                                                                                                               OR APPLICATION NUMBER: US 60/370,620
OR FILING DATE: 2002-04-04
BER OF SEQ ID NOS: 6077
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                                                                           291 CATGITTAACCGITCGICTTATTCAA 266
                                                                                                                                                                                                                                                                                                                                                                                                        PPLICATION NUMBER: US 60/325,448
ILING DATE: 2001-09-26
PPLICATION NUMBER: US 60/325,277
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Kreps, Joel
Provart, Nicholas
Ricke, Darrell
Zhu, Tong
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Cooper, Bret
Glazebrook, Jane
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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/ Cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
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6 NEW PUB.seq:*
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58.7	59.3	59.3	59.3	, 59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	59.3	60.0	60.0	60.0	60.0
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d	US-11-117-187-211	US-11-121-086-98	US-11-117-187-212	US-10-995-561-13295	US-10-995-561-13311	US-11-155-232-1	US-10-995-561-358	US-10-995-561-357	US-09-925-065A-704155	US-09-925-065A-704154	US-09-925-065A-704153	US-11-010-239-68	US-09-925-065A-716810	US-09-925-065A-667982	US-09-925-065A-673673	US-09-925-065A-673672	US-09-925-065A-826915	US-10-995-561-52210	US-10-995-561-9787	US-10-995-561-9774	US-09-925-065A-30379	US-09-925-065A-30378	US-09-925-065A-821053	US-09-925-065A-819344
Sequence 7828, Ap	e 211		Sequence 212, App		33	e 1	358				Sequence 704153,	œ				Sequence 673672,					Sequence 30379, A.	Sequence 30378, A		Sequence 819344,

ALIGNMENTS

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RESULT 2 US-09-925-065A-863989 Sequence 863989, Application US/09925065A, Publication No. US20040181048A1 GENERAL INFORMATION: GENERAL INFORMATION: JOA'D AND AND AND AND AND AND AND AND AND AN	Query Match Query Match Best Local Similarity 79.3%; Pred. No. 28; Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0; Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0; Qy 1 CATGCTTGTTCAACCGTTCGTTTGTTCC 29	RESULT 1 US-11-136-527-2272 Sequence 2272. Application US/11136527 Publication No. US20050287570A1 GENERAL INFORMATION: APPLICANT: Wyeth APPLICANT: Wyeth APPLICANT: Mounts, William M TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086) CURRENT APPLICATION NUMBER: US/11/136,527 CURRENT FILING DATE: 2005-05-25 PRIOR APPLICATION NUMBER: US 60/574,294 PRIOR FILING DATE: 2005-05-26 PRIOR FILING DATE: 2005-05-26 NUMBER OF SEQ ID NOS: 362830 SOFTWARE: PATENT NOS: 362830

Result No.

Score

Query Match Length DB

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Description

SUMMARIES

18 18 18 18 18 18

2 US-11-136-527-2272 US-09-925-055A-863899 US-09-925-055A-546217 US-11-197-133A-5 US-09-925-055A-472473 US-09-925-055A-936359 US-09-925-055A-936350 US-09-925-055A-953397

Sequence 2272, Ap Sequence 863989, Sequence 8646217, Sequence 5, Appl1 Sequence 936350, Sequence 936350, Sequence 936397, Sequence 933397, Sequence 86, Appl Sequence 86, Appl Sequence 811550, Sequence 772237, Sequence 772137, Sequence 772137, Sequence 772137, Sequence 772137, Sequence 7231, Appl

US-10-523-503-37 US-10-330-773-86 US-09-925-065A-811550 US-09-925-065A-772237 US-09-925-065A-72237 US-09-925-065A-72237 US-10-750-185-52713 US-10-750-185-64410 US-09-925-065A-70688 US-09-925-065A-70688

787145, 423, App 52713, A

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US-11-197-133A-5/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-546217
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-863989
                                                                                                                                                                                  RESULT 4
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PRIOR FILLING DATE: 2000-10-24
PRIOR PELLICATION NUMBER: US 60/252,147
PRIOR FILLING DATE: 2000-11-20
PRIOR FILLING DATE: 2000-11-30
PRIOR PELLICATION NUMBER: US 60/250,092
PRIOR FILLING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILLING DATE: 2001-01-16
PRIOR FILLING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
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                                   GENERAL INFORMATION:
APPLICANT: De Le Fuente Jose de Jesus
APPLICANT: Kocan Katherine M.
APPLICANT: Garcia-Almazan Consuelo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 546217
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                                                                                                                   Sequence 5, Application US/11197133A Publication No. US20060040361A1
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
TITLE OF INVENTION:
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FILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
FILING DATE: 2000-11-30
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                     Garcia-Almazan Consuelo Blouin Edwin F.
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Protective antigens and vaccines for the control of multi species
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Pred. No. 31;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Gen
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/252,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                             US-09-925-065A-472473/c
Sequence 472473, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-08-04
PRIOR APPLICATION NUMBER: US 10/972789
PRIOR FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: US 10/425563
PRIOR FILING DATE: 2003-04-29
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NAME/KEY: misc_feature
LOCATION: (1789)..(1789)
OTHER INFORMATION: n is a c g
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LOCATION: (1623)..(1623)
OTHER_INFORMATION: n is a c g
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LOCATION: (1606)..(1606)
OTHER INFORMATION: n is
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LOCATION: (1487)..(148
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LOCATION: (1762)..(1762)
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LOCATION: (1595)..(1595)
OTHER INFORMATION: n is
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SEQ ID NOS:
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US-09-925-065A-936360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 936359
                                        PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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SEQ ID NO 472473
LENGTH: 520
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                                                                                                                                                                                                                                                                                                                                                                                                              341 CATCCTTGCTCACCCTCTCGTCTTTGTCCA 370
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23; Conservative
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SEQ for Windows Version 4.0
                    2000-11-30
UMBER: US 60/261,766
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76.7%;
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Pred. No. 38;
0; Mismatches
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Pred. No. 37;
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LENGTH: 1908
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US-10-523-503-37/c
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Best Local S
Matches 23
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Best Local S
Matches 23
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Publication No.
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Publication No. US20040181048A1
                                                                                                                                           APPLICANT: BASF PLANT SCIENCE GMBH
TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS
FILE REFERENCE: 16313-0236
CURRENT APPLICATION NUMBER: US/10/523,503
CURRENT FILING DATE: 2005-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JUMBEN
SOFTWARE: Fa.
SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/.09/925,065A
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TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-99
NUMBER OF SEQ ID NOS: 957086
NUMBER OF SEQ ID NOS: 957086
NUMBER OF SEQ ID NOS: 957086
                                                                     IOR APPLICATION NUMBER: US 60/400,803
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PatentIn version 3.2
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23; Conservative
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o. US20060037102A1
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Pred. No. 38;
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Pred. No. 38;
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US-09-925-065A-811550
; Sequence 811550, Application US/09925065A
; Publication No. US20040181048A1
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, ORGANISM: Arabidopsis thaliana
US-10-523-503-37
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; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-86
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SEQ ID NO 86
LENGTH: 128963
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                             SEQ ID NO 811550
LENGTH: 599
TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-811550
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20
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APPLICANT: Marc Malandro
TITLE OF INVENTION: NOVel Compositions and Methods
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILLING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hums
FILE REFERENCE: 108827.135
                                                                                           PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                     APPLICATION NUMBER: US 60/250,092
FILING DATE: 2000-11-30
APPLICATION NUMBER: US 60/261,766
FILING DATE: 2001-01-16
                                                                                                                                                       APPLICATION NUMBER: US 60/289,846
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23; Conservative
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Pred. No. 1.5e
0; Mismatches
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Pred. No. 51;
0; Mismatches
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-01-16
PRIOR PRICATION NUMBER: US 60/261,766
PRIOR PRICATION NUMBER: US 60/261,766
PRIOR PRICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PRICATION NUMBER: US 60/261,766
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US-09-925-065A-772237
; Sequence 772237, Application US
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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US-09-925-065A-787145/c
; Sequence 787145, Application US/09925065A
; Publication No. US20040181048A1
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
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US-09-925-065A-772237
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 787145
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 108827.135
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; TYPE: DNA; Homo sapiens US-09-925-065A-787145

Query Match Best Local Similarity

61.3%; 78.6%;

Score 18.4; Pred. No. 60

DB 6; Length 629;

Mismatches

Indels

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2 ATGCTTGTTCAACCGTTCGTCTTGTTCC 29

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; ORGANISM: Homo sapiens
US-09-925-065A-423
PRIOR APPLICATION NUMBER: US 60/437,482
                                                                                                                                                                                                                                                                         equence 52713, Application US/10750185
blication No. US20050260603A1
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Local Similarity 78.6%;
hes 22; Conservative
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                                       ERENCE: MMI1100-2
APPLICATION NUMBER: US/10/750,185
                                                                    I: DeNISE, Sue K.

I: KERR, Richard

I: ROSENFELD, David

T: HOLM, Tom

T: BATTES, Stephen

T: PANTIN, Dennis

INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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IG DATE: 2000-11-30

CATION NUMBER: US 60/261,766

IG DATE: 2001-01-16

IG DATE: 2001-01-16

CATION NUMBER: US 60/289,846
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; TYPE: DNA ; ORGANISM: Bovine 19866881292329 US-10-750²185-52713

Query Match

61.3%; Score 18.4; 78.6%; Pred. No. 67

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454 ATTCTTGTTTAACCGTATTTCTTGCTCC 481

Search completed: March 6, 2006, 10:32:51 Job time : 31.3166 secs

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/mol_type="unassigned
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                    /organism="Zea mays"
/mol_type="unassigned
/db_xref="taxon:4577"
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                                                                                                                              GI:15554644
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100.0%; Pred. No. 0.0001;
tive 0; Mismatches 0
                                                                                                                                                       255 bp
Patent W00160997.
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Patent WO0160997,
              Fox, T.W.,
                                         Andropogoneae;
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.W., Garnaat, C.W., regulatory region
                                                                                                                                                                                                                                                                                                               Score 40; DB 6;
Pred. No. 8.6e-05;
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a; Poales; Poaceae; PACCAD
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 Huffman, G. and method
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Best Local Similarity
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PP 19-UN-1998 JP 1:
PR 23-UN-1997 US
PR 23-UN-1997 US
PI TIMMY L KENDALL
PC C12N15/82,C12N15
,C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Sit
CC Topology: Linear
FH Key
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  Homo
                           BD062177
BD062177.1 GI:22607782
JP 2001520523-A/2.
                                                                    BD062177 1394 bp Male tissue-preferred regulatory
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1 (bases I to 1394)
Albertsen,M.C., Fox,T.W., Garnaat,C.W.,
Kendall,T.L.
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JP 2001520523-A/1.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                Homo sapiens (human)
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23-JUN-1997 US 08/880499
MARC C ALBERTSEN,TIMOTHY W FOX,CARL W GARNAAT,GARY A HUFFWAN,
TIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
  sapiens
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30-OCT-2001
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Location/Qualifiers
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/ 100.0%; Pr
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Huffman, G.A.

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RESULT 8
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                                                                                     1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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Location/Qualifiers
1. 1394
                                                                                                                           40;
                                                                                                                                                                                                                                                                                                         Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Soermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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Sequence 1 from Patent
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         AX224395
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PD 30
PF 19
PF 19
PF 20
PF MB
PF 77
PC CC
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CC ST
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PN JP 2001520523-A/2
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Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G.A.
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(larity 100.0%; Pred. No. 6.;
Conservative 0; Mismatches
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Topology: Linear;
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23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFMAN,
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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AF360356
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Zea mays
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1 (bases 1 to 3343)

1 (Pox,T.W., Trimmell,M.R. and Albertsen,M.C. Cloning of Ms45, a gene required for male ferility from Zea mays
                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-MAR-2001) Trait and Technology Development, Pioneer Hi-Bred Intl. Inc., 7300 N.W. 62nd Ave., P.O. Box 1004, Johnston, IA 50131-1004, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Vagnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.
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AX224395
AX224395.1 GI:15554637
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ssue-preferred regulatory region and
WO 0160997-A 23-AUG-2001
HI-BRED INTERNATIONAL, INC. (US)
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/translation="mekrniqwrrgrdgivqyphlffaalalallyadffglsplaby
dyrfvkhelafygevmgswfrdnasrlrrgrlefvgevfgpesiefdlqgrgfyagla
dgrvrwmgbeagweffavmnpdwseevcangvnsttrkqhekeefcgrplglrfhge
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                                                         Coodon gtart=1
product="male fertility protein"
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oin(1392. .1768,1898. .2182,2280.
gene="M845"
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                                                                                                                                                                                                                                                                                                                                    organism="Zea mays"
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                                                                                                                                                                                                                                                                               db_xref="taxon:4577"
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APOO8209 053 APOO8209 054 APOO8209 055 APOO8209 056 APOO8209 056 APOO8209 056 APOO8209 066 APOO8209 067 APOO8209 077 APOOR209 077	RESULT 10 APORADO PASC NECONMENT Sequence split into 362 fragments LOCUS APDO8209 Accession APOR8209 Fragment Name Begin 1 10000 APOR8209 000 1 10000 1 20000 APOR8209 000 1 10000 1 110000 APOR8209 000 1 100000 1 110000 APOR8209 001 1 110000 1 110000 APOR8209 001 2 10000 1 200000 APOR8209 001 2 10000 2 10000 APOR8209 001 3 10000 3 10000 APOR8209 001 3 1000	TGELYVADAYYGLMVVGOSGGVASSVAREADGDPIRPANDLDVHRNGSVFFTDTSWRY SRKDHLNILLEGEGTGRLLRYDPETSGVHVVLKGLVFPNGVQISEDHQFLLFSETTNC RIMRYHLEGEGTGRLLRYDPETSGVHVVLKGLVFPNGVQISEDHQFLLFSETTNC RIMRYHLEGFPDAVGSNGRGQFWVAIDCCRTPAQEVFAKRPWLR TLYFKEPLSLKVLTWKARARWHTVLALLDGEGRVVEVLEDRGHEVMKLVSEVREVGRK LWIGTVAHNHIATIPYPLED" Query Match Best Local Similarity 100.0%; Score 40; DB 15; Length 3343; Best Local Similarity 100.0%; Pred. No. 5.4e-05; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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		FEATURES SOURCE		COMMENT	TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS TITLE	TITLE JOURNAL	REFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL	AUTHORS TITLE JOURNAL	ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS	SULT 1 135206	F & .	Query Match Best Local : Matches: 3
			>=30); ar as compre one plasm restricti 29427-328	On Jan 11 On Jan 11 This sequence we regions we chemistry	Saski,C., Sun,S. Direct Su Submitted	Submitted Arizona, 5 (bases Wing,R.A.	4 (bases Wing, R.A. Collura, F Direct Su	Direct Su Submitted Arizona,	Arizona, 3 (bases Wing, R.A.	2 (bases 1 Wing,R.A., Currie,J., Cirect Subm	Wing, R.A., Yu Collura, K. Rice Genomic Unpublished			AC135206	1 AGGATACCTACTCCAAACAATCCATCTTA	tch al Simi 34;
/clone="0J1041F02"	/organism="Oryz /mol_type="geno /db_xref="taxon /chromosome="3"	bclone. Areas 6995 5607, and 133052-13 e sequence of this Monsanto and Arizo Location/Qualifiers	sesions and id subclone on digest. The and at a least one one one of the subclone of the subcl	, 2003 this , 2003 this lence was fi ere either or covered	Saski, C., Henry, D., Tho Sun, S. Direct Submission Submitted (16-APR-2003)	mitted (11-JAN-2003 zona, 303 Forbes, T (bases i to 137327) g,R.A., Yu,Y., Sode	4 (bases 1 to 137327) Wing,R.A., Yu,Y., Soderlur Collura,K. and Thompson,S Direct Submission	Currey Corrura, North Control of	zona, 303 Forbes, T (bases 1 to 137327) g,R.A., Yu,Y., Sode	ses 1 to 137327) A., Yu,Y., Soderlur ,J., Collura,K. and Submission ted (09-OCT-2002) A	wic Sequence	Oryza sativa (japonica cultivo Oryza sativa (japonica cultivo Bukaryota; Viridiplantae; Str. Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza 1 (bases 1 to 137327)	Oryza Bativa (japonica OJ1041F02, complete seq AC135206 AC135206.3 GI:27596977 ACI35206.3 GI:27596977		CTACTCCCAA	76.0%; larity 85.0%; Conservative
L041F02"	/organism="Oryza sativa /mol_type="genomic DNA" /db_xref="taxon:39947" /chromosome="3"	single subclone. Areas 69957-70: 108316-105607, and 133052-133152 nucleotide sequence of this BAC of Syngenta, Monsanto and Arizona Gustation/Qualifiers	-30); an attempt was made to re as compressions and repeate; all one plasmid subclone; and the a restriction digest. There are tra 29427-32874 and at area 19945-33 by a single subclone; Region 186	too Jordan s sequence inished as double-str double	Thompson, S.	Submitted (11-JAN-2003) Arizona Arizona, 303 Forbes, Tucson, AZ 5 (bases 1 to 137327) Wing,R.A., Yu,Y., Soderlund,C.,	327) Soderlund,C., ompson,S.	Direct Submission Submitted (06-NOV-2002) Arizona Arizona, 303 Forbes, Tucson, AZ	Arizona, 303 Forbes, Tucson, AZ 3 (bases 1 to 137327) Windg.R.A., Yu.Y., Soderlund,C., Currie I Collura K and Thomps	<pre>2 (bases 1 to 137327) Wing,R.A., Yu,Y. Soderlund,C., Currie,J., Collura,K. and Thomps Direct Submission Submitted (09-0CT-2002) Arizona</pre>	Yu,Y., Soderlund,C., c Sequence	Oryza sativa (japonica cultivar- Oryza sativa (japonica cultivar- Bukaryota; Viridiplantae; Strept Spermatophyta; Magnoliophyta; Li Ehrhartoideae; Oryzaee; Oryza 1 (bases 1 to 137127)	Oryza sativa (japonica cultivar- OJ1041F02, complete sequence. AC135206 AC135206.3 GI:27596977 ACHTG. Cotting (japonica cultivar-	137327 bp	AGGATACCTACTCCCAAACAATCCATCTTA	; Score 30.4; 1; Pred. No. 0.11
		70761, 8983 70761, 8983 52 are cove C clone was Genomics I	y=30); an attempt was made to resolve all sequencing problems as compressions and repeats; all regions were covered by more one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area 29427-32874 and at area 19945-33212. Region 70511-70536 is coby a single subclone. Region 18678-18873 is a double stranded by a single subclone.	clemeon university, 100 Jordan Hall, Clemeon, 90 29034, USA On Jan 11, 2003 this sequence version replaced gi:24635991. This sequence was finished as follows unless otherwise noted: regions were either double-stranded or sequenced with an alte- chemistry or covered by high quality data (i.e., phred qualit	., Simmons,	റംഒ		peom,s. a Genomics II Z 85721, USA	Z 85721, USA , Kim,HR.,		, Kim, HR.,	ar-group, ar-group, eptophyta, E Liliopsida,	group)	AND Q	TACTCATGCAAC 40 .	.4; DB 15; . 0.18; tches 6;
	(japonica cultivar-group)"	761, 89836-90416, 98951-99009 are covered by Monsanto only clone was generated by combin enomics Institute sequencing	sequencing were covered confirmated at located at long 70511-70 on 70511-70 is a double	laced gi:2 laced gi:2 ess otherw quenced wii	Simmons,J., Thurmond,S.K. a. University Genomics Institut		Kim,HR., Rambo,T.,	Om,s. Genomics Institute, Universi 85721, USA	85721, USA Kim,HR., Rambo,T.,	Kim,HR., Rambo,T., Saski,C on,S. Genomics Institute, Universi	, Rambo,T., Currie,		chromosome 3	linear	C 40 .	Length 110000; Indels 0;
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sequence version replaced gi:24655891.
sished as follows unless otherwise noted: all
slowble-stranded or sequenced with an alternate
by high quality data (i.e., phred quality
smade to resolve all sequencing problems, such
repeats; all regions were covered by more than
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ere are transposons located at area
era 1945-33212. Region 70511-70536 is covered
Region 18678-18873 is a double stranded
Region 18678-18873 is a double stranded
ass 69557-70761, 98836-90416, 98951-99009,
3052-133152 are covered by Monsanto only. The
if this BAC clone was generated by combining
darizona Genomics Institute sequencing data. und,C., Kim,H.-R., Rambo,T., Saski,C., oultivar-group) unltivar-group) ; Streptophyta, Embryophyta, Tracheophyta; hyta, Lillopsida, Poales, Poaceae; Oryza. 37327 bp DNA linear PLN 16-APR-2003 :ultivar-group) chromosome 3 clone sence. und, C., Chen, M., Kim, H., Rambo, T., pson, S., Simmons, J., Thurmond, S.K. and Arizona Genomics Institute, University son, AZ 85721, USA Arizona Genomics Institute, University son, AZ 85721, USA und, C., Kim, H.-R., Rambo, T., id Thompson, S. Arizona Genomics Institute, University son, AZ 85721, USA und, C., Kim, H.-R., Rambo, T., Currie, J., und, C., Kim, H.-R., Rambo, T., Currie, J. Saski, C., e E of. 얁

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FFGGIDILQDYDITKKLEHAYKSFQVNPDYISAVDPKLYSRRFQDFIRRVFIKEQ"
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/note="unknown protein"
                                                                                                                                  complement (join (26563.
                                                                                                                                                                          /gene="OJ1041F02.4"
/note="unknown protein"
                                                                                                                                                                                                                                                                                                 complement (26563.
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ent(join(26563. .26772,27082. .27288,27430. .275:
.27940,28051. .28126,28327. .28484,28616. .28678,
.28874,29560. .30575))
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Matches 34
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/product="hypothetical protein"
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SKDEVILVDESPOKKQRKGRGKNQGAALKVPNRKHCKALBSTDGHESCQQLRSSQTQA
VLPQKS9TSVDIDLVTGPSEASPVNDNVDALNNEDKPQLIVDLRSEANIACHENTRLS
SGKKMHPFASARKIHKAGQOILNDEDEDMOSLCAFERDPPLCPVHVLYELEVTMPH
MSNKWLIADKSFLGTSTTEQNSAEHADPGKHLANFHDKQNKSKFSQDVIDUDDECLL
/note="putative MITE, Castaway-like"
complement (59793. .62196)
/gene="OJ1041F02.6"
                                                                                                                                                                                                                                                                                                            /note="putative MITE, MITE-adh,
39681. .39879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein"

complement (join (3504) . 35184,35866 . .36033,36922 . .3720;

37280 . .38523,40038 . .40104,40196 . .40287,40406 . .40617,

41678 . .41760,42229 . .42259,42907 . .43088,43694 . .43753,

41678 . .41760,42229 . .4259,42907 . .43088,43694 . .43753,

44229 . .44426,44622 . .44676,45877 . .45992,46149 . .46313,

46447 . .46620,47271 . .47470,47915 . .48019,48200 . .48263,

49589 . .49855))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGISDEGVFFAVKEVCLCDQGSNAQQCIFQLEQEIALLSQFEHENIVQYYGTDKEDSK
LYIFLELVTQGSLASLYQKVELRDTHYGSAYTRQILNGLTYLHENIVHRDIKCANILV
HANGSVKLADFEGLAKEIKFNVLKSKYKGTVYMFAPEVVDFKTTYGPEDDIMSLGCTV
HANGSVKLADFEGLAWTQALTKFNVLKSKYKGTVMFAPEVVDFKTYGPEDDIMSLGCTVL
EMLTRQLPYPGLEWTQALTKRICKGEPAIPNCLKSDARDFISQCVKFMPDDIMSLAKTU-
LEHPFVNRSMRSIRSMRTSSRSNSSILVLLIMMSWPGRTIRYREAILSTAQSSTFTIA
FHLLILSHSLLRGDMSWFSQRLIFSPENRLNVHSSA"
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AKETPRSVALEAPAFLLRVDDWEPARRDVRKASGEGGIKGVRPPDFVVLKRPESMVRPA
VCVVESTMDILRSPAPEEDSHAHAPAARSGGGDACQDAGEEEDDAAAVLILEELIKJES
TSEEFTGTSSLSTTNDDETSSTTTESMFYISPNGRFRRKIRSMNRGMLLGSGSFGTVF
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QsppaasapasgspslacspacsldltsfriggsgdgcrdvQllcsslglsgvddfav
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/protein_id="AAP06847.1"
/db_xref="GI:29893593"
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/codon_start=1
                                                                                                                                                                                                                                                     /note="putative MITE, MITE-adh, type G-like"
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2 (bases 1 to 303308)
Worley,K.C.
Direct Submission
Submitted (03-FEB-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor Co
Center code: BCM
Web site: http://
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Cow Genome Sequencing Consortium.

Direct Submission

Direct Submission

Submitted (01-JUL-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On JUN 28, 2005 this sequence version replaced gi:58531390.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig secaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.

Center: Baylor College of Medicine
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Center project name: FDUU
Center clone name: FDUU
Center clone name: FDUU
Center clone name: FUE40-60X24
Consensus quality: 284059 bases at least Q40
Consensus quality: 284059 bases at least Q20
Consensus quality: 284379 bases at least Q20
Batimated insert size: 289468; sum-of-contigs estimation
Duality coverage: 5x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

4449 4449 4481: contig of 4448 bp in length
4449 44481: contig of 9745 bp in length
14244 1429: gap of 50 bp
14244 1429: gap of 50 bp
14294 35369: contig of 12086 bp in length
14395: gap of 50 bp
14756 49432: contig of 12086 bp in length
14948 51615: contig of 12086 bp in length
14948 51615: contig of 6917 bp in length
15949 59488: gap of 50 bp
159489 59488: gap of 50 bp
164872 64871: gap of 50 bp
174540: contig of 50 bp
174541 74590: gap of 50 bp
174541 100066: contig of 973 bp in length
100451 104550: contig of 9213 bp in length
100451 104590: gap of 50 bp
104651 104650: contig of 1500 bp
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6: gap of 50 bp
8: contig of 6792 bp in length
6: gap of 798 bp
7: contig of 4471 bp in length
1: gap of 124 bp
1: gap of 124 bp
8: contig of 11967 bp in length
8: gap of unknown length
4: contig of 1126 bp in length
4: gap of unknown length
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1 (bases 1 to 55001)

1 (bases 1 to 55001)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Banks,T.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Alsbrooks,S.L., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Barbaria,J., Benton,J., Bimage,K., Brown,R., Bryant,N.P.,
           of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 28, 2002 this sequence version replaced of the control of the 
                                                                                                                                                                                                                                                                          Submitted (27-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 6 (bases 1 to 55001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are onl sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

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ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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/mol type="genomic DNA"
/db xref="taxon:9606"
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                                                                                                             /rpt family="MIR"
complement(4847. ,401")
/rpt family
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rpt_family="L1PA4"
                                                                                                                                                                                                                                                                                                                                                                   note="overlaps bases 177088. .178388 of clone AC079630" function="clone overlap"
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_family="L2"
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                                          family="AluSg"
lement(7309. .7
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ement(422)
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60.0%; Score 24; DB 84.4%; Pred. No. 62; vative 0; Mismatches	fami Temer	σ Ι (/rpt_family="(TAAAA)n" 2268222789	/rpt_tam11y="AluJb" 2263322680	เดเ		922680	Tement (20660	1913619158 /rpt family="AT rich"	ment (18855	18844.'.18854 /rpt family="AT rich"	<pre>complement(1830918606) /rpt_family="Alusx"</pre>	<pre>/rpt_family="AluJb"</pre>	Eamily="MIR"	/rpt_tamily="MIR" 1618616413	complement (1505815127)		œ	13737 family="AT 1	<pre>comptement(129/51308/) /rpt_family="FLAM_C"</pre>	family="(CA	/rpt_family="MIR" 1279712828	11217		, ۱۳۰	1091211015 /rpt family="1",1P"	1058710846 /rpt family="L1M4"	complement (91519317) /rpt_family="LTR43"	
8; Length 55001; 5; Indels (,																				•				

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KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT 14 AL807784/c LOCUS DEFINITION AL807784 127196 bp DNA linear ROD 13-NOV-2002 MOUSE DNA sequence from clone RP23-448C18 on chromosome X, complete HTG.
Mus musculus (house mouse)
Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; AL807784.11 GI:25045332

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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: RMBL; Sw.; SWISSEROT; Tr.; TRENEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep RP23-448C18 is from the RPCI-23 Mouse PAC Library constructed by the group of Pleter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                             Pan troglodytes BAC clone CH251-422M6 complete sequence.
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Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                     Pan troglodytes
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Direct Submission
Submitted (27-APR-2005) Washington University School of Medicine,
Serome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
                                                                                                                                                          On Mar 30, 2005 this sequence version replaced gi:59933404
                                                                                                                                                                                                                                                                                   Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                    Submitted (30-MAR-2005) (
Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                             Forest Park Parkway, St. 3 (bases 1 to 154857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-FEB-2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shah, N., Cotton, M. and Lewis, S.
The sequence of Pan troglodytes BAC clone CH251-422M6
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu
                           Contact: submissions@watson.wustl.edu
Center project name: C_AB0422M06
                                                                                                                                            ----- Genome Center
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. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                    Genetics, Genome Sequencing Center, Louis, MO 63108, USA
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TICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the Children's Hospital Oakland Research Institute, BACPAC Resources, by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0471; birthdate:6-6-80). The clone and detailed information can be obtained from Pieter de Jong and co-workers at http://www.bacpac.chori.org.

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Query Match
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                                             /note="Sequence
                                                                            note="Unresolved bases"
                                                                                                                                                       clone="CH251-422M6"
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/db_xref="taxon:9598"
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 60.0%;
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Maximum Match 100%
Listing first 45 summaries
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Ac138730 Rice Stre
Ac138730 Rice Stre
Ac138730 Rice Stre
Abz10202 Haematopo
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Aah76334 Z. mays M
Aah76340 Z. mays M
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The
                                                                                                                                                               A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
                                                                                                                                  Claim 14; Page 32; 50pp; English.
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-21.4 53.5 8168 6 As663328 21.4 53.5 24401 4 ABL03396 21.5 52.5 1531 14 ADM7938 21.5 52.5 1531 14 ADM7938 21.5 52.5 2000 11 ADV15965 22.5 2000 12 ADV15964 23.5 2.5 2000 12 ADV15964 24.5 2.5 2000 12 ADV15964 25.5 2000 12 ADV15964 25.5 2000 12 ADM15964 26.5 2.5 2000 12 ADM15964 27.5 2.5 2000 12 ADM15964 28.5 2.5 2000 12 ADM15964 29.5 2.5 2000 12 ADM15964 29.5 2.5 2000 12 ADM15964 29.5 2.5 2000 8 ABZ10206 29.5 2.5 2000 8 ABZ10206 29.5 2.5 8404 10 ADM15406 29.5 2.5 8404 10 ADM15406 29.5 2.5 8404 10 ADM154076 29.6 20.6 20.6 20.6 20.6 20.6 20.6 20.6 20				•			•
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ALIGNMENTS

RES	ARHTG337	
ID	AAH76337 standard: DNA: 40 BP	
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AC	AAH76337;	
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ij	29-OCT-2001 (first entry)	
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DE	 mays Ms45 male tissue-preferred regulatory region fragment. 	
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Ş	. Ms45; male tissue; regulatory region; transcription; male fertility.	
€ ₹	hybrid seed; ds.	
8	Zea mavs	
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PN	. WO200160997-A2.	
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B	23-AUG-2001.	
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y PF	13-FEB-2001; 2001WO-US004527.	
밁	15-FRB-2000 2000TG-00504/07	
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Y PI	Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL;	
3 !	WIT. 2001 614320/60	
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RESULT 3
AAH76334
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ID ANAPTG336

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Z. mays
                                                                                                                                                                                                                                                                                                                                                                                               comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -111 bases upstream of the TATA box of a Z. mays Ms45 male-tissue preferred regulatory region
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    mays Ms45 male tissue-preferred regulatory region fragment.

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23-AUG-2001. WO200160997-A2 hybrid seed;

promoter; ds

M845; male tissue; regulatory region; transcription; male

fertility;

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RESULT 4
AAH76340
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                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                            comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -38 to -195 bases upstream of the TATA box of a Z. mays M845 male-tissue preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hybrid seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ms45; male tissue; regulatory region; transcription; male fertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH76334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH76334 standard; DNA; 158
                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2000; 2000US-00504487
                                                                                                                                                    AAH76340;
                                                                                                                                                                                                                                                                                                                                                     nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PION-) PIONEER HI-BRED INT INC
                                                                                                                             29-OCT-2001
                                                                                                                                                                           AAH76340 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mays Ms45 male tissue-preferred regulatory region fragment
                                                                                                     mays Ms45 promoter fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                    86
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                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                   AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 47; 50pp; English.
                                                                                                                                                                                                                                    AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 125
                                                                                                                                                                                                                                                                                                                             158 BP; 41 A; 50 C; 21 G;
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                                                                                                                                                                                                                                                                               100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                             (first entry)
                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnaat
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                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ğ
                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                              46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huffman
                                                                                                                                                                                                                                                                                              5e-06;
                                                                                                                                                                                                                                                                                                        DB 5; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising nucleotide sequences the MS45 gene useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ō
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                                                                                                                                                                                                                                                                                   Gaps
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Best Local S
Matches 40
                                                                                                                                                 19-JUN-1998;
   The sequence is that encoding region. It may be used in the
                                            New nucleic acid encoding a - useful in mediating plant
                                                                         WPI; 1999-105628/09
                                                                                                                               23-JUN-1997;
                                                                                                                                                                    30-DEC-1998.
                                                                                                                                                                                                                        Ms45; male; tissue-preferred; plant tissue; differentiated;
                           Claim 2; Page 22-23; 39pp; English
                                                                                                             (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                      WO9859061-A1
                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                  Zea mays Ms45 male tissue-preferred regulatory region
                                                                                                                                                                                                                                                                        08-JUN-1999
                                                                                                                                                                                                                                                                                                            AAX07408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 255 BP;
                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                   AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
                                                                                                                                                                                                                                                                                                                                                      AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 138
                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                       (first
                                                                                           Fox
                                                                                                                               97US-00880499.
                                                                                                                                                98WO-US012895
                                                                                                                                                                                                                                                                                                                                                                                                                             59 A; 86 C; 39 G; 71 T; 0 U; 0 Other;
                                                                                           ,WT
                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                           1394
                                                                                           Garnaat CW,
                                          M845 male tissue-preferred regulatory region fertility, especially hybrid seed production.
                                                                                                                                                                                                                                                                                                                                                                                           <u>,</u>
                                                                                                                                                                                                                                                                                                           ВP
an Ms45 male tissue-preferred regulatory construction of a vector for a method of
                                                                                                                                                                                                                       regulatory region; plant cells;
maize; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                         Huffman GA,
                                                                                                                                                                                                                                                                                                                                                                                                   5.3e-06
                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                         Kendall TL;
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1239

AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC Query Match Best Local S Matches 40

1 Similarity 40; Conserv

100.0%;

Score 40; DB Pred. No. 6.8 0; Mismatches

6.8e-(DB 2;

40 Indels Length 1394;

0,

Gaps

0

0

Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;

plants

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RESULT 6
AAX07409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 40
The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolB and diptheria coxin. Hybrid seeds are produced by cross-pollinating maize male fertile
                                                                                                                                                                Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                New nucleic acid encoding a - useful in mediating plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ms45; male; tissue-preferred; plant tissue; differentiated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring fertility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably which encodes a product selected from auxins, rolB and diptheria toxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
                                                                                                                                                                                                                                                                                          Albertsen MC,
                                                                                                                                                                                                                                                                                                                                                              23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9859061-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX07409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX07409 standard; DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998.
                                                                                                                                                                                                                                                                                                                            (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                        Fox TW,
                                                                                                                                                                                                                                                                                                                                                              97US-00880499.
                                                                                                                                                                                                                                                                                                                                                                                                98WO-US012895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue-preferred regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                          Garnaat CW,
                                                                                                                                                                                              Ms45 male tissue-preferred regulatory region fertility, especially hybrid seed production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory region; plant cells; hybrid seed; fertility; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                        Huffman GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1394;
                                                                                                                                                                                                                                                                                        Kendall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a Z. mays Ms45 promoter fragment

of.

A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.

comprising nucleotide sequences the MS45 gene useful for

WPI; 2001-514772/56

15-FEB-2000;

(PION-) PIONEER HI-BRED INT INC

Fox TW,

Garnaat CW,

Huffman G,

Kendall TL;

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13-FEB-2001; 2001WO-US004527

Example 5; Fig 8; 50pp; English.

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RESULT 8
AA1763
ID AA417
XX AA417
XX AA477
XX AA
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AAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 martissue preferred regulatory region from Z. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A male tissue-preferred regulatory region comprising nucleotide essential for initiating transcription of the MS45 gene useful f mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH76332 standard; DNA; 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z. mays Ms45 male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-2000; 2000US-00504487
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        WO200160997-A2
                                                                                                                                                                                 hybrid seed;
                                                                                                                                                                                                                    M845; male tissue;

    mays Ms45 male tissue-preferred regulatory region encoding DNA.

                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH76333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH76333 standard; DNA; 1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                             entry)
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                                                                                                                                                                                                                    region;
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                                                                                                                                                                                                                         transcription;
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                                                                                                                                                                                                                                         ss; abiotic agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an MS45 martissue preferred regulatory region from Z. mays
                                                                                         22-JUN-2001;
24-AUG-2001;
26-SEP-2001;
21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A male tissue-preferred regulatory region essential for initiating transcription of mediating fertility in a male plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1394 BP; 411 A; 309 C; 232 G; 442 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 47; 50pp; English.
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                                                                                                                                                                                                                                                                               Rice stress-regulated promoter SEQ ID NO:17293
                                                                                                                                                                                                                                                                                                     02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                  ACL38730 standard; cDNA; 2000 BP.
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                                                                                                                                                                                                                      Oryza sativa
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                                             Kreps J,
                                                                                                                                                  21-JUN-2002; 2002WO-US019668
                                                                                                                                                                          30-JAN-2003.
                                                                                                                                                                                               WO2003008540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                     SYNGENTA PARTICIPATIONS
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                                 Briggs SP,
T, Provart
                                                                                         2001US-0300112P.
2001US-0314662P.
2001US-0325277P.
2001US-0332132P.
                                                                                                                                                                                                                                                        stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                 Cooper B,
N, Ricke
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Pred. No.
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G
                                   Glazebrook J,
D, Zhu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising nucleotide sequences the MS45 gene useful for
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RESULT 10
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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynuclectides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, compotic stress or any of their combinations. The present sequence is a composite of the invention of the invention
                                                                                                                                                  Claim 1; SEQ ID NO 1948; Opp; English.
                                                                                                                                                                                  Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                                                                                   WPI; 2003-328604/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genomic sequence hCG1639824.
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85.0%;
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Pred. No. 0.
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RESULT 11
ABZ10202/c
ID ABZ10
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AC ABZ10
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AC ABZ10
XX
The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a complete with at least 1 gene and/or their regulatory regions in a biological sample obtained from the subject with at least 1 research, which distinguishes between methylated and non-methylated CDG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 CCC which distinguishes between methylated and non-methylated CDG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 CCC represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative CCC disorder haematopoietic cells; for differentiating between acute 1 jmphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related DNA amplification of haematopoietic cell proliferation disorder related DNA
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                                                                                                                                                                                                                                                                                                                                                     Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA genes are useful as DNA vaccines and the CAP are useful as TNA vaccines and the CAP are useful as TNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published Sequence 226215 BD. CTO.
                                                                                                                                                                                                                                                                                                                      Claim 28; SEQ ID NO 342; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-018942/01.
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29; Conservative
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P, Grabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller J;
ne R, Leu E,
, Otto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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RESULT 12
ABL32304/c
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Best Local S
Matches 24
Query Match
Best Local Similarity
                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabettic; antisporiatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                  Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4110 BP; 945 A; 0 C; 1132 G; 2033 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                         diagnosis ar
methylation.
                                                                                                                                                                                                                                                                                       Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL32304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL32304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                      Claim 1; SEQ ID NO 277; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune
                                              Sequence 6309
                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                     EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                    Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACCTAACCCCAAACAATCCATCCTAC 3056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATACCTACTCCCAAACAATCCATCTTAC 31
                                                                                                                                                                                                                                                                      cid comprising and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      system associated gene SEQ ID NO: 277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                              BP; 1758 A; 69 C; 1364 G; 3118 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
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54.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6309
                                                                                                                                                                                                                                                                      fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                       Berlin
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Pred. No. 1.6e
0; Mismatches
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Score 21.6;
Pred. No. 1.
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 .6; DB 6;
. 1.7e+02;
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             Length 6309,
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RESULT 13
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                                                            S
                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for detecting and differentiating continuous colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at cleast one reagent or a series of reagents, where the reagent or series of creagents, distinguishes between methylated and non methylated CG dinucleotides within the target nucleic acid. The molecules of the created convertion demonstrate cytostatic acityty whilst the method may useful convention demonstrate cytostatic acityty whilst the method may useful converting and differentiating between colon cell proliferative colorers, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid) oligomers are useful as probes for converting cytosine methylation state or single nucleotide cytosine cytosine methylation state or single nucleotide cytosine c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
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Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 32; SEQ ID NO 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-731620/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2002; 2002EP-00004551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pretreated
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                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                        specification
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3083
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                                                                                                                                                                      Similarity
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AAACCTAACCCCAAACAATCCATCCTAC 3056
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                                                            ATACCTACTCCCAAACAATCCATCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burger M,
Schmitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic DNA region
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                                                                                                                                                                                                                                                                     BP; 1818 A; 0
                                                                                                                                                                                                                                                                                                                                            is taken
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                                                                                                                                                                                                                                                                                                                                        from Wipoweb.
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                                                                                                                                  Score 21.6; D
Pred. No. 1.7e
0; Mismatches
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                                                                                                                                                                                                                                                                        C; 1721 G; 3571 T; 0 U; 0 Other;
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                                                                                                                                      Gaps
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RESULT 14 ADE84196/c

ADE84196 standard; DNA; 7110 BP.

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The invention relates to a method of detecting and differentiating C Detween lymphoid cell proliferative disorders associated with at least cone gene and/or their regulatory regions in a subject by contacting a ct target nucleic acid in a biological sample obtained from the subject with C at least one reagent or series of reagents that distinguish between CC methylated and non-methylated CPG dinuclectides within the target nucleic cacid. The genes and/or their regulatory regions are preferably selected CC from MDR1, CSNKEB, EGR4, AR, CDK4, RB2, CDC25A, GPID betra, MYOD1, CDM3, CC MYCL1, ELK1, ABL1, APC, BC12, CDH1, CDKNIA, CDKNIB, CDKNIA, CDKNIB, COK ABL1, APC, BC12, CDH1, CDKNIA, CDKNIB, CDKNIC, CC GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RB12, TGFBR2, TP73, CDKNIC, CC GSKIBbetra, ESR1, APAR1, BAK1, BAK, BAX OF HOXAS. Oligomers, peptide nucleic code the genes are useful for detecting the methylation state on the sequences CC of the genes are useful for detecting the methylation state of all the CC goldunclectides within one or more the sequences, or their complements, CC for determining the cytosine methylation state and or single nuclectide conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, CC lymphoma. They are also useful for detecting of a predisposition to, CC differentiation between subclasses, diagnosis, prognosis, treating and/or conditioning of lymphoid cell proliferative disorder. This sequence conditioned cannot cell of a pretreated genomic DNA derived from the mentioned genes.
       Ś
                                                                                      Query Match
Best Local S
Matches 24
                                                                                 Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; SEQ ID NO 192; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diffuse large B-cell lymphoma; mant chronic lymphocytic leukemia; small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; lymphoid cell proliferative disorder; methylation;
methylated CpG dinucleotide; single nucleotide polymor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
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4 ATACCTACTCCCAAACAATCCATCTTAC 31
                                              Similarity
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                                 Conservative
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                                                                                                               genes.
                                           54.0%;
85.7%;
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                                <u>,,</u>
                                            Score 21.6;
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                                 Mismatches
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                                                         10;
                                4;
                                                       Length 7110;
                                Indels
                              0;
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                              Gaps
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Best Local S
Matches 24
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RESULT 15
ADS89580/c
ID ADS89580 standard; DNA; 7:
XX
AC ADS89580;
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DT 18-NOV-2004 (first entry
XX
   Foekens J,
Nimmrich I,
                                                                                                                                                                                                                                                                                        ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
                                                                                   01-OCT-2002; 2002DE-01045779.
07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
                                                                                                                                                                                                                                                           Unidentified.
                                                                                                                                                       01-OCT-2003; 2003WO-EP010881.
                                                                                                                                                                                                                                                                                                                                           Oligonucleotide of the invention SEQ ID NO:596.
                                                                                                                                                                                                                          WO2004035803-A2.
                                                      EPIG-) EPIGENOMICS AG
 Harbeck N, Rujan T,
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   Koenig
Schmitt
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 ÞΉ
Maier S, Martens J,
Schmitt M, Look MP,
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Predicting responsiveness of a subject with breast cell proliferative disorder, useful for treating or differentiating breast cell proliferative disorders comprises analyzing methylation pattern of a genomic DNA from the subject.

Disclosure; SEQ ID NO 596; 104pp; English.

The invention relates to a novel method for predicting the responsiveness to a far subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligoners are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is used in the aversulfication of the breast tissues to a therapy. The present sequence is used in the exemplification of the invention.

Sequence 7110 BP; 1818 A; 0 C; 1721 G; 3571 T; 0 U; 0 Other;

4 ATACCTACTCCCAAACAATCCATCTTAC 31 Similarity ANACCTAACCCCAAACAATCCATCCTAC 3056 Conservative 54.0%; 85.7%; Score 21.6; D Pred. No. 1.7e 0; Mismatches 0 DB 13; Length 7110; Indels 0, Gaps

0

Search completed: March Job time : 26.619 secs 5 2006, 18:11:42

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3083

ANACCTANCCCCANACANTCCATCCTAC 3056

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Title: US. Perfect score: 40	Run on:	OM nucleic - nu
US-10-713-381-2_COPY_1239_1278 40	March 5, 2006, 18:11:59; Search time 188.843 Seconds (without alignments) 9910.279 Million cell updates/sec	OM nucleic - nucleic search, using sw model

Sequence: 1 aggatacctactcccaaacaatccatcttactcatgcaac 40

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : gb_est1:*
gb_est2:*
gb_est3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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220	17	15	12	9	76	0 W 4 R	No.
22.6	22.8	223	23.2	23.2 23.2 23.2	23.8	35.2 34.2	Score
56.5	57.0	57.5 57.5	58.0 57.5	58.0 58.0	59.5	100.0	Query Match
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1221	. ω ω κ	277	φ δ	7 10	ဖှစ	10 910	9 13
AW257178 BE205271 CR843833	BM406466 DN570622	CJ037346 CJ035837 BG506830	CD495749 AZ883408	CC117589 CR181951 CL109241	H24137 BZ706605	CG224225 CC656933 CW324514 CW445575	ID CC656939
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CR843833 GROAAA78D	BF143726 601789606 BM406466 EST580781 DN570622 92287550		CD495749 CDA18-D05 AZ883408 RPCI-23-1	CO117589 GR Eb01H CR181951 Reverse s CL109241 ISB1-51D1	H24137 ym50g08.r1 BZ706605 SM416B1-G	CG224225 OG1AG08TV CC656933 OGWDQ20TM CW324514 104 819 1	Description CC656939 OGWDQ20TV

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55.5	55.5	55.5	55.5	55.5	55.5	55.5	55.5	55.5	55.5	55.5	55,5	56.0	56.0	56.0	56.0	56.0	56.5	56.5	56.5	56.5	56.5	56.5
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CL084441	CG383910	CZ727957	CG811817	CK949745	BM027586	AI382034	BF601210	AI467879	AA725064	AI698201	AI206216	CN317130	CK871857	CK864514	DT054853	BB264116	CL058859	CR818130	AW687128	AZ400686	CR843905	BZ173201
μ,		CZ727957 OC	CG811817 FSAAM35TR	CK949745 4074916 B	BM027586 GIT00010		BF601210 266128 MA	AI467879 tj78e09.x	AA725064 ai06h07.s	AI698201 wa67g11	AI206216 gr27f06.x	CN317130 AGENCOUR	CK871857 AGENCOUR	CK864514 AGENCOUR	DT054853 AGENCOUR	BB264116 BB264116	CL058859 CH216-88P	CR818130 GR0AAA43	AW687128 NF006C08R	AZ400686 1M0167P01	CR843905 GR0AAA79A	BZ173201 CH230-369

ALIGNMENTS

C CC656939 N OGMOQ20TV ZM 0.7 1.5 KB Zea mays genomic clone ZWMEWAOS5 OGMOQ20TV ZM 0.7 1.5 KB Zea mays genomic clone ZWMEWAOS5 CC656939 CC656939 CC656939.1 GI:32060231 GSS. Zea mays Embaryota; Viridiplantae; Streptophyta; Embryophyta; Tra Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poacea clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 687) Whitelaw,C.A. Quackenbush,J., Van Aken,S., Utterback,T. Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohl Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N. Consortium for Maize Genomics Umpublished (2002) Other GSSs: OGWDQ20TM Contact: Cathy Whitelaw TIGR Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Pax: 301-838-5843 Pax: 301-838-5843 Pax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: Tr Class: methylation filtered. Location/Qualifiers 1687 //Clone="Embason:4577" //Clone=#Embason:4577" //Clone=#Embason:4577 //Clone=#Embason:45	Query Match Best Local : Matches 4:	ORIGIN	FEATURES BOUICE	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 CC656939/c
N-2003 N-2003 TT.,	atch 100.0%; Score 40; DB 9; Length 687; cal Similarity 100.0%; Pred. No. 4e-05; 40; Conservative 0; Mismatches 0; Indels 0; Gaps	/organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /db_clone="Zexon:4577" /clone="Zexon:4577" /clone_1ib="ZM_0.7.1.5_KB" /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 methylation filtered genomic DNA library"	Contact: Cathy Whitelaw TIGR 71GR 9712 Medical Center Drive, Rockville, MD 20850, 9713 001-838-984 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: FF Class: methylation filtered. Location/Qualifiers 1. 687	Resnick, A., Fraser, C.M., Budiman, M.A., Citek, R.W., Nunberg, A., Robbins, D. and Consortium for Maize Genomics Unpublished (2002). Other GSSs: OGWDQ20TM	Elkaryota; Viridiplantae; Streptophyta; Emby Spermatophyta; Magnoliophyta; Liliopsida; Piclade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 687) Whitelaw, C.A., Quackenbush, J., Van Aken, S.,	W COMUÇAUTV ZM_0.7_1.5 KB Zea mays genomic Cione genomic survey sequence. CC656939 CC656939.1 GI:32060231 CC6589.1 GI:32060231 GSS. Zea mays	CC656939 687 bp DNA line

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CC656933
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                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidaee; Andropogoneae; Zea.

1 (bases 1 to 963)

1 (bases 1 to 963)

1 (bases 1, 0 gackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
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WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OG1AG08TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays
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/clone="Jib="ZM 0.7_1.5_KB"
/notee="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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|strain="B73"
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                                                                                                                                                                                                                              Tel: 314 615 6979
Fax: 314 615 5975
Email: jbedell@oriongenomics.com
Plate: 819 row: c column: 19
Seg primer: SWfor Forward
Class: methylation filtered
High quality sequence stop: 702.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilioppida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 702)

1 (bases 1 to 702)

Bedell, J. A., Budiman, M. A., Nunberg, A., Citek, R. W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B. A., Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J. A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CW324514 702 bp DNA linear GSS 31-OCT-2004 104 819_11477203_148_35910_078 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                   Orion Genomics, LLC
4041 Forest Park Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bicolor (sorghum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Bedell JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     15660154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), e13 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CW324514.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martienssen,R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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/clone=1bb="ZM 0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
/note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
prepared from purified nuclei was randomly sheared,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic Di
/strain="B73"
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                                                                                                                           /organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="ATx623"
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                                                         /clone_lib="Sorghum methylation filtered library (LibID:
                                                                                   /db_xref="taxon:4558"
/clone="11477203"
                                                                                                                                                                                                                Cocation/Qualifiers
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37; Conservative
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4041 Porest Park Ave, St. Louis,
Tel: 314 615 6979
Pax: 314 615 5975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CW445575 296 bp DNA linear GSS 02-NOV-2004 fsbb001f170m16k0 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone fsbb001f170m16, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: k Reverse
Class: methylation filtered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum genome sequencing by methylation filtration PLOS Biol. 3 (1), el3 (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Bedell JA
                                                                                 AGGATACCTACTCCCAAACAAT-CCATCTTACTCATGCAAC 40
                                          AGGACACCTACTCCCAAACAATCCCATGTTACCCATGCAAC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jbedell@oriongenomics.com
                                                                                                                                                                                                                                                                                         /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="Sorghum methylation filtered library (LibID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:4558"
clone="fsbb001f170m16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Sorghum bicolor"

mol_type="genomic DNA"

cultivar="ATx623"
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                                                                                                                                                      Score 24.2; D
Pred. No. 75;
0; Mismatches
                                                                                                                                                         0;
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                                                              RESULT 7
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H24137
LOCUS DEFINITION
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source
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AUTHORS
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                                                                                                                                                                                                                                 346 AAATCTACTCTCAAACATTTCATCTTATACATGCA
BZ706605 375 bp DNA
SM416B1-G07_55_13.abl Spider Monkey genomic
geoffroyi genomic, genomic survey sequence.
BZ706605
                                                                                                                                                                                                                                                                     4 ATACCTACTCCCAAACAATCCATCTTACTCATGCA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
Insert Size: 1161
High quality sequence stops: 349
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@inage.lnl.gov) for further information.
Insert Length: 1161 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 bp mRNA linear EST 06-
ym50g08.rl Soares infant brain 1NIB Homo sapiens cDNA clone
IMAGE:51939 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13RP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Location/Qualifiers
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//lab_host="DHIOB (ampicillin resistant)"
//lab_host="DHIOB (ampicillin resistant)"
//lab_host="DHIOB (ampicillin resistant)"
//lab_nost="DHIOB (ampicillin resistant)"
//lab_nost="DHIOB (ampicillin resistant)
/
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/mol_type="mRNA"
/db_xref="GDB:424875"
/db_xref="taxon:9606"
/clone="IMAGE:51939"
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                                                                                                                                                                                                                                                                                                                                          Score 23.8; DB 8;
Pred. No. 1.2e+02;
0; Mismatches 7;
                                                       DNA linear GSS 18-MAY-2003
genomic BAC library Ateles
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REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 GGATATCTACTTGTGAACCATACATTTTACTNAAGCAAC 217
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tu
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Qian Y, Jin L, Su B. Center for Genome Information University of Cincinnati Kettering Lab, 3223 Eden Ave., Tel: 1-513-558-6678
                                                                                                                                                             Gossypium raimondii
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 738)
1 (bases 1 to 738)
Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
                                                                                                                                                                                                                                                                                                                                                                                                   CO117589
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Construction and characterization of bacterial artificial chromosome library of black-handed spider monkey (Ateles geoffroyi) Genome 47 (2), 239-245 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae; Atelinae, Ateles.

1. (bases 1 to 375)
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                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
CO117589
CO117589.1 GI:48816276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ateles geoffroyi (black-handed spider monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BZ706605.1
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T7
Class: BAC ends.
                                                                                                                  Unpublished (2004)
                                                                                                                                   Global assembly of Cotton
                                                                                                                                                                                                                                                                                                        Gossypium raimondii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: subn@ucmail.uc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   Eb01H15.r GR_Eb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-513-558-4505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Fibroblast"
/cell_line="AG05352"
/dev_stage="3 DA"
/clone=lib="Spider Monkey genomic BAC library"
/clone="Vector: pBACe3.6; Site_1: EcoRI; Genomic
partially digested with EcoRI. Vector, pBACe3.6,
Recombinants were transformed into DH10B. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="black-handed spider monkey"
/db_xref="taxon:9509"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Ateles geoffroyi"
|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                     Gossypium
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Pred. No. 1.4e+02;
0; Mismatches 10;
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raimondii
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                                       ΑZ,
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                                         85721-0036, USA
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                                                                                                                                                                                                                                                                                                                                                                                                     linear
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CR181951
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             ISB1-51D14_Sp6.1 1
genomic survey sec
CL109241
CL109241.1 GI:400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR181951.1 GI:49960800 GSS; genome survey sequence; MICER. Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-FEB-2004) Sanger Centre, Hinxton, CB10 1SA, UK. http://www.sanger.ac.uk/MICER Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR181951 783 bp DNA linear GSS 06-JUL-20 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN361p21, genomic survey sequence.
                                                               CL109241
ISB1-51D14_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams,D.J., Biggs,P.J., Cox,A.V., Jonkers,J., Smith,J., Plumb,R.W., Rogers,J., and Bradley,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                  ATACCTACTCTAAGCCAATGCATCTTACTCCAGGAA 549
                                                                                                                                                                                        ATACCTACTCCCAAACAATCCATCTTACTCATGCAA
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="GR_Eb"
/clone_lib="GR_Eb"
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
EcoRV; Library made by Invitrogen wIth RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80
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Location/Qualifiers
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/dev_stage="_3 to +3 |
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="teaxon:29730"
/clone="GR_Eb01H15"
                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:10000"
/clone="MHPN361p21"
/clone_lib="MHPN"
                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                  GI:40602876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.0%;
                                                                                                                                                                                                                                                58.0%;
                                                               ISB1 Xenopus
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Pred. No. 2.2e-
0; Mismatches
                                                                                                                                                                                                                               Score 23.2; DB 11 pred. No. 2.2e+02; 0; Mismatches 8
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Taylor,R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'HPRT insertion targeting
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                                                                genomic
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Nishijima,I., Yu,Y.,
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                                                                    clone
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EST.
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanfor
Tel: 650 725 5954
Fax: 650 725 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD495749 MRNA Linear EST 12-JUN-2003
CDA18-DD5.yld-s SHGC-CDA Gasterosteus aculeatus cDNA clone
CDA18-D05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus tropicalis (western clawed frog) Xenopus tropicalis
                                                                                                                                                              High quality sequence start: 15
High quality sequence stop: 667.
Location/Qualifiers
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Actinopterygii; Neopterygii; Teleostei; Euteleostei
Acanthomorpha; Acanthopterygii; Percomorpha; Gaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 72 High quality sequence stop: 524.
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
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                                                                                                                                                                                                                                                                                                               Plate: 18
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                                                                                                                                                                                                                                                                                                                                            kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kingsley, DM
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/mol_type="genomic DNA"
/db_xref="txon:8364"
/clone="ISB1-51D14"
/clone_lib="ISB1"
/clone_lib="ISB1"
/clone_lib="ISB1"
/clone_Toganism="type:"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,C., Carter,J., McPherson,J., Warren,W., and Wilson,R.
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Salinas river, CA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to 1253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23.2; DB 10;
Pred. No. 2.3e+02;
D; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanford, CA 94305-5329, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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AUTHORS
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AZ883408/c
LOCUS
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ORGANISM
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KEYWORDS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ883408
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    /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="RPCI-23-189L2"
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the lacZ promoter of pBK-CMV. An amplified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for EST sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: lambda ZAP Express/pBK-CMV; Site_1: EcoR1 [5' adaptor]; Site_2: XhoI [3' linker primer]; The mixed organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a a 50 bp linker primer containing an oilgo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoRI cohesive end. The finished cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="mixed male and female"
tissue_type="heads and inte
                                                                                                                                                                                                                                                                                                                                                    re inserted in to the ZAP express vector
                                 58.0%;
Score 23.2; DB 6; Length 1253; Pred. No. 2.4e+02; 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal organs combined"
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1047 TACCTCTTTCCCAACAATCCATCTTCACCATCCAAC 1082 AZ883408 405 RPCI-23-189L2.TJ RPCI-23 Mus musculus DNA genomic linear mic clone GSS 05-MAR-2001 RPCI-23-189L2,

0;

0

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurograthi, Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 405) Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., Mus musculus AZ883408.1 GI:13202353 Mus musculus (house mouse) enomic survey sequence

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Pax: 301 838 0208 Other_GSSs: RPCI-23-189L2.TV and Fraser, C.M. End Sequences from Library RPCI-23

de

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pdejong@mail:cho.org). Clones may be purchased from BACPAC Resources (http://www.clori.org/bacpac/orderingframe.htm). BAC end page: http://www.clori.org/bab/bac_ends/mouse/bac_end_intro.html Plate: 189 row: L column: 2 Class: BAC ends mail: szhao@tigr.org POCHE ion/Qualifiers

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RESULT 13
CJ037346
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AUTHORS
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VERSION
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                                           Matches
                                                                                   Query Match
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                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CJ037346 linear 662 bp mRNA linear CJ037346 full-length enriched swine cDNA library, scrofa cDNA clone TES01G080111 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                         29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: huenishl@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 Ikenodai, Tsukuba,
Tel: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEDE (Pig EST Data Explorer): construction of a derived from porcine full-length cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Okumura,N., Hamasima,N. and Awata,T.
                                                                                                                                                                                                                                                                                                                                                            Š.
                                                                                                                                                                                                                                                                                                                                                                                                 Vector sequences were eliminated by RepeatMasker version 2002/07/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Hirohide Uenishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14681463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 32 (1), D484-D488 (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 662)
                                                                                                                                                                                                                                                                                                                                    quality bases were trimmed Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  crossmatch version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      +81-29-838-8627
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                                         Conservative
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//lab host="DH10B"
//clone lib="RPCI-23"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                              /tissue_type="testis"
/dev_stage="adult"
/clone_lib="full-length
testis"
                                                                                                                                                                                                                                                /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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                                                                                                                                                                                                                                 clone="TES01G080111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.5%;
74.4%;
                                                           57.5%;
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                                       Score 23; DB Pred. No. 2.6e.
                                         0;
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Pred. No. 2.4e+02
0; Mismatches 1
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                                                                                                                                                                    enriched swine
                                                                                   DB 7;
                                                               .6e+02;
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                                                                              Length 662;
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adult testis Sus
                                       <u>,</u>
                                                                                                                                                                    library,
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                                         Gaps
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ORGANISM
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CJ035837
LOCUS
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VERSION
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                                                                                             KEYWORDS
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                                                                                                                                                                                                                                                                                             609
                                                                                                                               mRNA sequence.
BG506830
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CJ035837 full-length enriched swine cDNA library,
scrofa cDNA clone TES01E060090 5', mRNA sequence
CJ035837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
Outleic Acids Res. 32 (1), D484-D488 (2004)
                                                      Homo sapiens
                                                                                                                                                                 BG506830 798 bp n
601861443F1 NIH_MGC_77 Homo sapiens
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Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Kenodai, Teukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
Hominidae; Homo.
                                                                        Homo sapiens (human)
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74.4%;
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Pred. No. 2.7e+02;
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                                                                                                                                                                                                      222 ACTCCCAAACCAGCCTTCTTAGTCATGCATC 192
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/mol_type="mRNA"
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/clone="Ibb="NIH_MGC_77"
/clone="lib="NIH_MGC_77"
/clone=lib="NIH_MGC_77"
/clone
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                                                                                                                                         US-09-949-002-7790/c
                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                        US-08-880-499-2
     GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08880499 Patent No. 6037523
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                                                                                                  Sequence 7790, Application US/09949002
Patent No. 6900016
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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FILE REFERENCE: CL000790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sweeney, Patricia A. REGISTRATION NUMBER: 32,733 REFERENCE/DOCKET NUMBER: 05. TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 800
ATTORNEY ACCESS.
                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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STREET: Box 1000
CITY: Johnston
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 50131
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STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
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100.0%; Pr
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Pred. No. 6e-
0; Mismatches
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                             DISEASE, METHODS OF DETECTION
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; ORGANISM: Human
US-09-949-002-7790
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; ORGANISM: Human
US-09-949-002-7791
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US-09-248-796A-5546
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, N
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO0790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
CURRENT FILING DATE: 2000-01-28
                                                                                                                                                                                                                                                                                                          Sequence 5546, Appli
Patent No. 6747137
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7790
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Best Local Similarity
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                                                                           SEQ ID NO 5546
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CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
                                                                                                              FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILIAGNION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                     APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                            NUMBER OF SEQ ID NOS: 28208
            LENGTH: 1071
TYPE: DNA
ORGANISM: Candida albicans
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74.3%;
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Pred. No. 51;
O; Mismatches
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Pred. No. 51;
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; ORGANISM: Human
JS-09-949-016-14995
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Best Local Similarity 74...
Conservative
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SEQ ID NO 14995
LENGTH: 42075
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                                                                  Matches
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Patent No. 6812339
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PRIOR FILING DATE: 2000-10-20
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CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                                                         PLICANT: VENTER, J. Craig et al.
TLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ent No. 6900016
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TLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TLE OF INVENTION: WITH INCLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION TILE OF INVENTION: AND USES THEREOF
                                                                Local Similarity 85.2
es 23; Conservative
 31591 ATTCCTACCCACAAACCATCCATCTTA 31565
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                              4 ATACCTACTCCCAAACAATCCATCTTA 30
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                                                                             51.5%;
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                                                                0; Mismatches
                                                                                 Score 20.6;
Pred. No. 1
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                                                                                              DB 3; Length 42075;
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                                                                Indels 0;
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                                               ; NAME/KEY: CDS
; LOCATION: (231)..(749)
US-09-774-528-184
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Query Match
Best Local Similarity
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Patent No. 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                             SOFTWARE: PU
SEQ ID NO 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-774-528-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-949-016-65770,
                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                    FEATURE:
                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                    REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184,
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                                                                                                                                                                                                                                                                    INVENTION:
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                                                                                                                                                                                  pt_FL_genes Version 2.0
                                                                                                                                                                                                                                                                                                          Wehrman, Iom
Wang, Jian-Rui
Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09774528
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                                                                                                                                                                                                                                                                                                                                                 Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chenghua
di, Vinod
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h. Ryle
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Yonghong
                                                                                                                                                                                                                                                          No. 67436176.
Polypeptides
 51.0%;
71.1%;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 65770
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         414 ĠĠATTĊĊTGGGĊTĊAAGĊAATĊĊTCĊTGCĊTĊAGĠĊAA 377
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                                                                                                                                                                                                                                                                                                                                                                                              : Drmanac, Radoje T.
INVENTION: No. 6743619el Nucleic Acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09949016
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Score 20.4; DB 3; Length 973; Pred. No. 68;
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APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6919193el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT APPLICATION NUMBER: 09/774,528
PRIOR APPLICATION NUMBER: 09/774,528
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
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Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 973
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (231)..(749)
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Coupland, GAPPLICANT: Putterill,
                                                      CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                      APPLICATION NUMBER: PCT/0
FILING DATE: 01-NOV-1995
                                                                                      FILING DATE: 20-OCT-1997
                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                        STREET: 8th Flog
                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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          APPLICATION
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                                                                                                                                                                                                                        Virginia
7: United States of America
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Ren, Feiyan
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                                                                                                                                                                                                                                                                           3: Nixon & Vanderhye PC
8th Floor, 1100 No. 6077994th Glebe Road
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71.1%;
                                          PCT/GB95/02561
                                                                                                           US/08/945,056
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RESULT 13
US-09-949-016-17420
; Sequence 17420, Application US/09949016
; Patent No. 6812339
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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ORIGINAL SOURCE:
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; LOCATION: (1)...(51770)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13668
                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13668
LENGTH: 51770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13668, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: Landsberg erecta
POSITION IN GENOME:
MAP POSITION: Chromogo-
-945-056-4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
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9851 GGATTCCTGGGCTCAAGCAATCCTCCTGCCTCAGGCAA 9814
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                                2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
                                                                         Similarity 71.1
27; Conservative
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71.1%;
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Pred. No. 92;
                                                                         Score 20.4; DB 3;
Pred. No. 1.6e+02;
0; Mismatches 11;
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                                                                                                               Length 51770;
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POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF,

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                                                                                                     Query Match
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                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: VENTER, J. Craig et al.
TILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n = A, T, C or G
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OCATION: (1)...(84571)
                                                                                                                                                                                                                        GANISM: Human
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53133 GGAAATCAACTCCAAAAAGGAACCTTCAAAATCATGCAA 53096
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                                                                                                                                                                                                                                                                              NO 11
                                                                                                                                                     INFORMATION: n = A, T, C or G
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                                                               l Similarity 71.1
27; Conservative
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27; Conservative
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                             GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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                                                                                 51.0%;
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71.1%;
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                                                                               Score 20.4;
Pred. No. 1.
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Pred. No. 1.7e+02;
0; Mismatches 11; Indels 0;
                                                                               9e+02
                                                                                               DB 3; Length 126200;
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RESULT 15

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                                                              Query Match 51.0
Best Local Similarity 71.1
Matches 27; Conservative
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53133 GGAAATCAACTCCAAAAGGAACCTTCAAAATCATGCAA 53096
                                2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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OLYMORPHISMS IN KNOWN GENES ASSOCIATED
יידייי יידיאא DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                     51.0%; Score 20.4; DB 71.1%; Pred. No. 1.9e+tive 0; Mismatches
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Search completed: March 5, 2006, 22:36:28
Job time : 11.1834 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /cgn2 6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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US-10-713-391-2
US-10-713-993-680
US-10-424-599-31006
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US-09-925-055A-670302
US-10-424-599-83179
US-10-424-599-83179
US-10-424-599-83179
US-09-925-055A-591011
US-09-925-055A-59103
US-09-925-055A-59103
US-09-925-055A-29323
US-09-925-055A-29323
US-09-925-055A-293339
US-10-473-126-342
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US-10-713-381-5
US-10-713-381-3
US-10-713-381-9
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                                            Sequence 6, Appli
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Sequence 1, Appli
Sequence 2, Appli
Sequence 31006, Ap
Sequence 670302,
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Sequence 1948, Ap
Sequence 591012,
Sequence 591012,
Sequence 591013,
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Sequence 253727,
Sequence 33427,
Sequence 33437,
Sequence 33447, App
Sequence 377, App
Sequence 377, App
Sequence 281837,
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Sequence 6, Application US/10713381 Publication No. US20040221331A1 GENERAL INFORMATION:

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US-10-311-455-1568	-10 - 473	-10-473-126-198	-10-041-018-362	US-10-041-018-361	10-260-238-2594	10-424-599-20320	US-09-925-065A-937247	US-09-925-065A-285328	US-09-925-065A-285327	US-09-925-065A-285326	US-10-424-599-24043	US-10-312-841-2	US-10-312-841-1	US-11-097-143-2335	JS-10-240-454-23	JS-10-311-455-901	JS-10-240-452-4	-10-311-455-128	-09-938-842A-1555	-09-938-842A-1555	-09-925-065A-6316	
1-4	3-1	3-1	1-0	1-0	0-2	4-5	5-0	5-0	5-0	5-0	4-5	12-	12-	97-	0-4	1-4	0-4	1-4	8-8	8-8	5-0	
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ALIGNMENTS

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CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 40
TYPE: DNA
ORGANISM: Zea mays
US-10-713-381-6
                                              Sequence 5, Application US/10713381
Publication No. US20040221331A1
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: HUFFMAN, GARY
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
                                                                                                                                                                                                                                                  RESULT 2
US-10-713-381-5
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Best Local S
Matches 40
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APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARLAR, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF THE STREET SAME
FILE REPERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
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FILE REFERENCE: 578R

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CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
ORGANISM: Zea mays
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US-10-713-381-3
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Publication No. US20040221331A1
GENERAL INFORMATION:
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Best Local Similarity
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Best Local :
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Publication No. US20040221331A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARWART, CARL W.
APPLICANT: HUFFMAN, GARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                        APPLICANT: ALBERTSEN, MARC C. APPLICANT: FOX, TIMOTHY W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                86 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 125
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Pred. No. 5.2e-06;
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LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-9
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10713381
Publication No. US20040221331A1
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Best Local Similarity
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                                SOFTWARE: F
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APPLICANT: GARNAAT, CARL W.

APPLICANT: HUFFWAN, GARY

APPLICANT: KENDALL, TIMMY L.

TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF

TITLE OF INVENTION: USING SAME
                                                                APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFWAN, GARY
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 578R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
TYPE: DNA
                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           1239 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 1278
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                                                     PatentIn
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Pred. No.
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US-10-719-993-6880/c
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US-10-713-381-2
                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_128002C.1
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Tocal Similarity
Tonger
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 31006
LENGTH: 706
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Best Local Similarity 84.4%;
Matches 27; Conservative
                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                   APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FRASESEQ for Windows Version 4.0
EQ ID NO 6880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001496
                                                                                                                                                                          ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: La Rosa Thomas J
PPLICANT: Kovalic David K
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blication No. US20040265849A1
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LOCATION: (1)...(85779)
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5 TACCTACTCCCAAACAATCCATCTTACTCATGCAAC 40
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                                                                                 Similarity
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                                                            58.0%;
ilarity 77.8%;
Conservative
                                                       ; Score 23.2; DI
; Pred. No. 39;
0; Mismatches
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                                                                                               DB 7; Length 706;
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226 ATACCTGGTCCCATACACTCCATCTTACT 254

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OTHER INFORMATION: Clone ID: MRT4577_62049C.1 US-10-425-115-143168
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US-10-425-115-143168
                                               Query Match
Best Local Sim
Matches 25;
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Publication No. 1
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Best Local :
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                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2003-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-925-065A-670302/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                    LE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with LE OF INVENTION: Plants
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4 ATACCTACTCCCAAACAATCCATCTTACT 32
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                                               Similarity 86.2
25; Conservative
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US20040214272A1
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                                                               56.5%;
86.2%;
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                                             Score 22.6; D
Pred. No. 56;
O; Mismatches
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Pred. No. 4
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US-09-925-065A-591011/c
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LENGTH: 315
TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1948, Application US/10087192 Publication No. US20020182586A1 GENERAL INFORMATION:
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                                                              Sequence 591011, Application US/09925065A publication No. US20050228172A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1948
LENGTH: 226215
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Best Local
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000112
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR TILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2059
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APPLICANT: Engelhard, Eric
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72.5%;
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                                                                                                                                                                                                                                                                                                  Score 22.4; DB 5;
Pred. No. 2.5e+02;
0; Mismatches 11
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RESULT 14
US-09-925-065A-591012/c
; Sequence 591012, Application US/09925065A
; Publication No. US20050228172A9
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PRILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2011-01-16
PRIOR PRILING DATE: 2011-01-16
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-01-16
PRIOR PRILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-591012
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 591011
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
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CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24
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ORGANISM: Homo sapiens
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351
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                              14 CCAPACAATCCATCTTACTCATGCAAC 40
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  CCAAACAAACCACCTTACTCATGCAGC 325
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Pred. No. 94;
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Pred. No. 94;
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RESULT 15 US-09-925-065A-591013/c

Sequence 591013, Application US/09925065A Publication No. US20050228172A9 GENERAL INFORMATION:

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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION UNDER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR TILING DATE: 2001-130
PRIOR APPLICATION NUMBER: US 60/25,147
PRIOR APPLICATION NUMBER: US 60/25,146
PRIOR APPLICATION NUMBER: US 60/25,092
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/25,946
PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086
US-09-925-065A-591013
US-09-925-065A-591013

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Match
Best Local Similarity 88.9%; Pred. No. 94;
Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;

Ouery Matches 24; Conservative 0, Mismatches 3; Indels 0; Gaps 0;
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time : 59.5163 secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
2 6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
2 6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
5 6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

; GENERAL INFORMATION:	Sequence 62555, A	8 US-10-750-623-62555	52.5 1718	21	c 20	
; Publication No. US20050260603A1	Sequence 62555, A	8 US-10-750-185-62555	52.5 1718	21	c 19	
; Sequence 58624, Application US/10750185	Sequence 937247,	6 US-09-925-065A-937247	52.5 653	21	c 18	
US-10-750-185-58624	Sequence 285328,	6 US-09-925-065A-285328	52.5 617	21	17	
RESULT 2	Sequence 285327,	6 US-09-925-065A-285327	52.5 617	21	16	
	Sequence 285326,	6 US-09-925-065A-285326	52.5 617	21	15	
	Sequence 24503, A	12 US-11-124-367A-24503	52.5 201	21	14	
Db 474 AGGAAACGGATTAACAAACTATCCACCTT	Sequence 63167, A	6 US-09-925-065A-63167	53.5 653	21.4	13	
	Sequence 189248,	6 US-09-925-065A-189248	53.5 620	21.4	c 12	
Qy 1 AGGATACCTACTCCCAAACAATCCATCTT	Sequence 281838,	6 US-09-925-065A-281838	53.5 560	21.4	. 11	
	Sequence 281837,	6 US-09-925-065A-281837	53.5 560	21.4	10	
Matches 29; Conservative 0; Mismato	Sequence 393490,	6 US-09-925-065A-393490	54.0 598	21.6	0	
Similarity 74.4%;	Sequence 888321,	6 US-09-925-065A-888321	55.0 628	22	Ω α	
Query Match 57.5%; Score 23;	Sequence 253727,	6 US-09-925-065A-253727	55.5 613	22.2	. 7	
	Sequence 591013,	6 US-09-925-065A-591013	55.5 611	22.2	6	
US-09-925-065A-670302	Sequence 591012,	6 US-09-925-065A-591012	55.5 611	22.2	0	
; ORGANISM: Homo sapiens	Sequence 591011,	6 US-09-925-065A-591011	55.5 611	22.2	0	
; TYPE: DNA	Sequence 58624, A	8 US-10-750-623-58624	56.5 3242	22.6	. (
; LENGTH: 636	Sequence 58624, A	8 US-10-750-185-58624		22.6	· N	
; SEQ ID NO 670302	Sequence 670302,	6 US-09-925-065A-670302	57.5 636	23		
; SOFTWARE: FastSEQ for Windows Version 4.0			į			
; NUMBER OF SEQ ID NOS: 957086	Description	DB ID	Match Length DB	Score !	No.	
; PRIOR FILING DATE: 2001-05-09			Query		Result	

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51.0	51.0	51.0		μ	51.0	51.0	51.0		51.0	51.0	51.0	51.0	51.0	51.0	51.0	μ	51.5	μ	μ	51.5		N	52.0	52.0	
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US-09-925-065A-575923	US-09-925-065A-575922	US-09-925-065A-573143	US-09-925-065A-104305	US-09-925-065A-910942	US-09-925-065A-659195	US-09-925-065A-785033	US-09-925-065A-241631	US-09-925-065A-166725	US-09-925-065A-589114	-065A	US-09-925-065A-589112	US-09-925-065A-589111	US-09-925-065A-951077	US-09-925-065A-360599	US-10-995-561-70646	US-09-925-065A-696033	US-09-925-065A-696032	US-09-925-065A-610819	US-09-925-065A-127036	US-11-175-859-103341	US-10-750-623-57406	US-10-750-185-57406	US-10-750-623-49907	US-10-750-185-49907	
Sequence 575923,	Sequence 575922,	Sequence 573143,	Sequence 104305,	Sequence 910942,	Sequence 659195,	Sequence 785033,	Sequence 241631,	æ	Sequence 589114,	Sequence 589113,		o	Sequence 951077,	æ	Sequence 70646, A	Sequence 696033,	Sequence 696032,	Sequence 610819,	Sequence 127036,	Sequence 103341,	57406,	٠,	Sequence 49907, A	Sequence 49907, A	

ALIGNMENTS

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TYPE: DNA
ORGANISM: Homo sapiens
JS-09-925-065A-670302
                                                                                                                                   Query Match 57.5%; Score 23; DB 6; Length 636; Best Local Similarity 74.4%; Pred. No. 11;
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 670302 LENGTH: 636
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                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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474 AGGARACCGATTRACARACTATCCACCTTTCTCAAGCAA 436
                                                                                                          29; Conservative
                                  1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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RESULT 4
US-09-925-065A-591011/c
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; ORGANISM: Bovine
US-10-750-623-58624
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PRIOR FILING DATE: 2003-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 58624
LENCTH. 2003-12-31
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                                                         GENERAL INFORMATION:
                                                                             Sequence 591011, Application US/09925065A Publication No. US20040181048A1
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PACENTIN VERSION 3.1
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 58624, Application US/10750623 
Publication No. US20050287531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MMI GENOMICS, INC. APPLICANT: DeNISE, Sue K. APPLICANT: KERR, Richard
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APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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0; Mismatches
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Pred. No. 23;
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-05-09
PRIOR FILING DATE: 2001-05-09
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; Sequence 591012, Application US/09925065A
; Publication No. US20040181048A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 591011
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LENGTH: 611
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Best Local
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CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
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PRIOR APPLICATION NUMBER: US 60/250,092
                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/261,766
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/252,147
                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
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351 CCAAACAAACCACCTTACTCATGCAGC 325
                    14 CCAAACAATCCATCTTACTCATGCAAC 40
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0; Mismatches
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Pred. No. 22;
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Pred. No. 22;
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RESULT 6
US-09-925-065A-591013/c
US-09-925-065A-591013/c
; Sequence 591013, Application US/09925065A
; Publication No. US20040181048A1

GENERAL INFORMATION:

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RESULT 8
US-09-925-065A-888321/c
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US-09-925-065A-591013
                                                                                                                           Matches
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SEQ ID NO 253727
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-09-925-065A-253727
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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TLE OF INVENTION: I
TLE OF INVENTION:
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                                                          292 GGAAATCAACTCCAAAASAAACCCTCAAAATCATGCA 328
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                                                                                    2 GGATACCTACTCCCAAACAATCCATCTTACTCATGCA 38
                                                                                                                        27; Conservative
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                                                                                                                      Score 22.2; D
Pred. No. 22;
1; Mismatches
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Pred. No. 22
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; TYPE: DNA; Homo sapiens US-09-925-065A-393490
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US-09-925-065A-888321
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                                                                                               Query Match
Best Local
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Best Local :
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Publication No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: Wang, David G.
TILE OF INVENTION: Identification and Mapping of Single
TILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/261,766
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/250,092
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/243,096 FILING DATE: 2000-10-24
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APPLICATION NUMBER: US 60/250,092
FILING DATE: 2000-11-30
228 TATCTSCTCTCAATCAATCCATCTTACT 201
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                                 5 TACCTACTCCCAAACAATCCATCTTACT 32
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NG DATE: 2001-05-09
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Pred. No. 27;
0; Mismatches
                                                                                           Score 21.6;
Pred. No. 38
                                                                         Mismatches
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US-09-925-065A-281837

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                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PAPPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELICATION NUMBER: US 60/261,766
PRIOR PELICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
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Publication No. US20040181048A1
                                           Matches
                                                                                   Query Match
                                                                                                                            LENGTH: 560
TYPE: DNA
ORGANISM: Homo sapiens
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hume
FILE REFERENCE: 108827.135
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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28; Conserv
  1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39
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Pred. No. 4
                                         Score 21.4; DB Pred. No. 46; O; Mismatches
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                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-63167
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; ORGANISM: Homo sapiens
US-09-925-065A-189248
                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-16
PRIOR FILING DATE: 2001-01-16
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Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 189248
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Best Local (
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                  Query Match
Best Local Similarity
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PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
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Pred. No. 47;
  Score 21.4;
Pred. No. 47;
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186 AGGAAACCTACACCCTGACATGTCAACTACTACTGCAA 224

1 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAA 39

28; Conservative

0; Mismatches 11; Indels

Gaps

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Sec. 14 . Sec. 3. 1. 1. 1. 2.

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RESULT 15
US-09-925-065A-285326
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US-11-124-367A-24503
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US-11-124-367A-24503
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Best Local Similarity 73.0
Matches 27; Conservative
Query Match
Best Local Similarity
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                                                                   ORGANISM: Homo sapiens
-09-925-065A-285326
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION |
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: "Accidentide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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RIOR FILING DATE: 2004-05-07
RIOR APPLICATION NUMBER: US 60/582,609
RIOR FILING DATE: 2004-06-25
RIOR FILING DATE: 2004-06-25
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blication No. US20060024700A1
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ID NO 24503
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LE OF INVENTION: Genetic Polymorphisms Associated with
LE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
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G DATE: 2004-08-09
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R: US 60/289,846
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  Score 21; DB 6; Length 617; Pred. No. 68;
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Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps

Oy 4 ATACCTACTCCCAAACAATCCATCCTTACTCCATGCAAC 40
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387 ATACATACTTCCAAACAATCCAGAGTTTTGTAGCAAC 423

Search completed: March 6, 2006, 10:32:52 Job time: 42.7555 secs

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Title:
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157
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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AC135206 Oryza sat
AX224398 Sequence
BX501854 Zebrafish
AC1104134 Homo sapi
CR847532 Danio pre
EX640577 Zebrafish
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20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.6	20.8	20.8	20.8	20.8	20.8	20.8	20.9	20.9	20.9	20.9	20.9	20.9	20.9	20.9	21.1	21.1	21.1	
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AC157998 Mus muscu	AC147437 Gallus ga		AL731779 Mouse DNA	AC159811 Mus muscu	Continuation (6 of	Mus mu	BC055469 Mus muscu		BC020027 Mus muscu	AC097405 Rattus no		N	Zebra	AC147308 Pan trogl	AC099973 Mus muscu	AC149044 Pan trogl	AC019229 Homo sap	AC087485 Homo sapi	AC135350 Homo sapi	AL121875 Human DNA	AC135264 Homo sapi	AC006602 Homo sapi		AC146134 Pan trogl	AC091864 Homo sapi	AC011290 Homo sapi	

ALIGNMENTS .

Oy , 121 CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC	OY 61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCAAACAATCCATCTTACTCATG	Qy 1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC	Query Match 100:0%; So Best Local Similarity 100.0%; Pa Matches 157; Conservative 0;	source 1255 /organism="Zea mays" /mol_type="unassigned /mol_type="taxon:4577" /db_xref="taxon:4577"	PIONEER HI-BRED INTERNATIONAL, FEATURES Location/Qualifiers	AUTHORS ALDERTSEN, M.C., FOX, T.W., GATHBAE, C.W., Huttman, G. TITLE Male tissue-preferred regulatory region and method JOURNAL Patent: MO 0160997-A 9 23-AUG-2001;	Eukaryota; Viridiplantae; Streptop Spermatophyta; Magnoliophyta; List Clade; Panicoideae: Andromogoneae;	SOURCE Zea mays ORGANISM Zea mays	VERSION AX224402.1 GI:15554644 XEYWORDS	DEFINITION Sequence 9 from Patent WO0160997 ACCESSION AX224402	RESULT 1 AX224402 LOCUS AX224402
	AGAGGATACCTACTCC 	TACATGCTTGTTCAAC 	Score 157; DB 6; Pred. No. 5.6e-40; Mismatches 0;	mays" Bigned DNA" :4577"	IONAL, INC. (US)	<pre>Fox, T.W., Garnaat, C.W., Huttman, G. ferred regulatory region and method 997-A 9 23-AUG-2001;</pre>	; Streptophyta; E hyta; Liliopsida; noogoneae: Zea.		•	00160997.	255 bp DNA
157 171	CAAACAATCĆATCTTI CAAACAATCCATCTTI	CGTTCGTCTTGTTCC	; Length 255; 10; 0; Indels 0;				Embryophyta; Tracheophyta;; Poales; Poaceae; PACCAD				linear PAT
	ACTCATG 120	ATCGTCC 60	Gaps 0;			and Kendall,T.L. of using same	acheophyta; ae; PACCAD				10-SEP-2001

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REFERENCE
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PD J0-OCT-2001

PR 23-JUN-1997 US 08/880499

PI TIMMY L KENDALL

PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC C C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC R01H5/00

CC Strandedness: Single;
CC Topology: Linear;
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Albertsen,M.C., Fox,T.W., Garnaat,C.W.,
Kendall,T.L.
                                                                                                                                                                                         Homo sapiens (human)
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Male tissue-preferred regulatory
BD062177
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Male tissue-preferred regulatory region Patent: JP 2001520523-A 2 30-OCT-2001; PIONBER HI BRED INTERNATIONAL INC PN JP 2001520523-A/2
                                                                                                                                                                                                                                   JP 2001520523-A/2.
                                                                                                                                                                                                                                                   BD062177.1 GI:22607782
                                                                                      1 (bases 1 to 1394)
Albertsen, M.C., Fox, T.W.,
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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19-JUN-1998 JP 1999504910
23-JUN-1997 US 08/880499
MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFWITIMMY L KENDALL
C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
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100.0%; Pred. No. 5.6e-40;
tive 0; Mismatches 0;
                                                                                            Garnaat, C.W.,
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PF 19-JUN-1998 JP 1999504910

PR 23-JUN-1997 US 08/880499

PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUF

PI TIMMY L KENDALL

PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00

C07K14/34,C12Q1/68,

PC A01H5/00

CC Strandedness: Single;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;
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AX224394
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                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poalea; Poaceae; PACCAD
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Pred. No. 5.6e-40;
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Sequence 2
AX224395
                                                                                                                                          Direct Submission Submitted (13-MAR
                                                                                                                                                                                                                                                                 Eukaryott, Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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Zea mays male fertility
AF360356
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                                                                                                           Hi-Bred Intl. Inc., IA 50131-1004, USA
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Eukaryota; Viridiplantae; Streptophyta; Em

Spermatophyta; Magnoliophyta; Liliopsida;

Clade; Panicoideae; Andropogoneae; Zea.
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protein
                                                                                                                        and Technology Development, Pioneer 62nd Ave., P.O. Box 1004, Johnston,
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a; Poales; Poaceae; PACCAD
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a; Poales; Poaceae;
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                                                                                                                                                                                                                                                   Albertsen, M.C., Pox.T.W., Garnaat,C.W., Male tissue-preferred regulatory region Patent: WO 0160997-A 3 23-MIG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US) Location/Qualifiers 1.158
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AX224396 158 bp
Sequence 3 from Patent W00160997.
AX224396 AX224396.1 GI:15554638
                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopseida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                          CGTGTCATCTCACATGCATACTACATGCTTGTTCAACCGTTCGTCTTTGTTCCATCGTC 60
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                                                                                                                          Conservative
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RIMRYMLBGPRAGEVEVFANLPGFPDNVRSNGRGQFWVAIDCCRTPAQEVFAKRPMLR
TLIFKFPLSLKVLTMKAARMHTVLALLDGBGRVVEVLEDRGHEVMKLVSEVREVGRK
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DGRVVRWMGEEAGWETFAVMNPDWSEEVCANGVNSTTRKQHEKEEFCGRPLGLRFHGE
TGELYVADAYYGLMVVGQSGGVASSVAREADGDFIRFANDLDVHRNGSVPFTDTSWRY
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/gene="M845"
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gene="M845"
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                                                                                                                        Score 146; DB 6;
Pred. No. 2.1e-36;
0; Mismatches 0
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	/gene="OJ10	. (36303		cerregeratrecegaaceaaceaceracreceaaacaareacecreacreareaa	CTACTCCCAAA	CAACAGAACÁC	GCTATTCCGAAC	36362 CCTT
	/note="(jap	gene		ACTCATGCAA 123	CCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCCAAACAATCCATCTTACTCATGCAA	CTACTCCCAAA	CAAGAGGATAC	CCTATTCTGAAC	64 CCTTC
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	/organism="Oryza sativa (Japonica cultivar-group)" /mol_type="genomic DNA"			30,	Length 110000;	DB 15;	; Score 54;	34.4%;	Match
	rce Location/C	FEATURES SOU					19610000	19500001	P008209_195
	nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics Institute sequencing data.						19410000	193,00001	P008209_193 P008209_194 ·
	single subclone. Areas 6957-70761, 89836-90416, 98951-99009, 105316-105607, and 133052-133152 are covered by Monsanto only. The						19210000	19100001	
	29427-32874 and at area 19945-33212. Region 70511-70536 is covered by a single subclone. Region 18678-18873 is a double stranded						19010000	18900001	111
	one plasmid subclone; and the assembly was confirmed by restriction digest. There are transposons located at area						18810000	18700001	008209_187 008209_188
	s=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than	•					18610000	18500001	
	regions were either double-stranded or sequenced with an alternate					`,	18410000	18300001	008209_183
	On Jan 11, 2003 this sequence version replaced gi:24635891. This sequence was finished as follows unless otherwise noted: all	COMMENT				•	18210000 18310000	18100001	
	Submitted (16-APR-2) Clemson University,	JOURNAL					18010000	17900001	
•	Sun,S. Direct Su	TITLE				•	17810000	17700001 17800001	9008209_177 9008209_178
		AUTHORS					17610000	17500001	008209_175
	5 (bases 1 to 137327)	REFERENCE					17510000 -	17400001	J. J.
·	-	JOURNAL		-			17310000	17200001	08209-172 08209-173
	Collura,K.	TITLE					17110000	17000001)08209_170)08209_171
		AUTHORS			•	.•	17010000	16900001	008209_169 008209_169
•	Arizona, 303 Forbes	JOURNAL					16710000	16600001	البالبا
	Direct Submission	TITLE					16610000	16500001	008209_165
	Wing, R.A.,	AUTHORS					16410000	16300001	1 1
	Arizona, 303 Forbes, Tucson, AZ 85721, USA						16210000	16100001	1 1
	Direct Submission	TITLE					16010000	15900001	1 1
	Wing, R.A., Yu, Y., Sc	AUTHORS		•		^	15810000	15700001	008209_157
	Nice demonite sequence The control of the control o	JOURNAL				١.	15610000	15500001	008209 155
	Collura, K.						15410000	15300001	1 1
		REFERENCE					15210000	15100001	0008209 151
	Spermatophyta; Magnolophyta; Liliopsida; Poales; Poaceae;			•			15010000	14900001	1 1
		ORGANISM			•			14700001	1 1
	HTG. Oryza sativa	KEYWORDS SOURCE					14610000 . 14710000	14500001 14600001	008209 <u>145</u> 008209 <u>146</u>
		ACCESSION VERSION					14410000	14300001	08209_143 08209_144
		DEFINITION		•			14310000	14200001	08209_141
	AC135206 137327 bp DNA linear	LOCUS LOCUS					14110000	1400001	1 1
		3					13910000	13800001	008209_138
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Query Match
Best Local Similarity 85.7
Matches 60; Conservative

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Geedvasiafedellespapllogbsvrsivoperlevniperdsilavosogleinirooaloiism
Lvkekaselkokkutjeiloywopcplitetadeodgsblaadbsaaeulotmatulpeh
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SAPDIDKKIRALKKKIRLAEAQVQGDPENLKPEQLEKMKKIEGMKEELKLLENKSSPA
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EGSKTTPPHHSVDFRWGVCPAAFFLIKHLRSYYEHVRQVKSTLLITRFYGTHCIKQAGCP
KIHRREDLKGSSHGRTIDKTERKIDETTTLKDLDLQVAFRLQRFWYEELMKGJQMDCT
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19263. .19454
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                                                      CTTCCATGCA 133
                                                                                                                   CCTTGGCTATTCCGAACCAACAGAACACCTACTCCCAAACAATCACGCTGACTCATGCAA
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ASSSCFHASLFESKOHERVOHELEFVTPKGCOTANLATDKORKFSSQDVIDVDECLL
ASSSCFHASLFESKOHERVOHELFFVTPKGCOTANLATDKYRPETAAOVCGNSKHYKF
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KSAAVFACAAERQGFNV I ELINPKTIVVF PF I PHIKLLAQTLDLKEDKLHDSSHPS I KY I
PTRVFVHMRINS I I SI SAHSSSLSVI KLHCLVNTSDKENGAYVROKFEEATKSHCLEK
WSQEEI I GLLPI SNISLDPAGTTPGTAEYKQVINKTL ILFEDVDTVFDEDRGFI STILKM
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QKKKQMEVSEFEGLELQIMTPLTKGRSAGKTRKPKKSKLKHGRSADCNDAS PCKNDLD
DFHDSPDI FLPSNHQMRNIRGCVLLFAESDDDLADAHAAKDATTFVQEGRILPGSSSL
PCLYGHGISNI VPESVFFQQSSVPHLHREVISI SQLCPPSSRAFEPASSFQNQLESOM
PGSI SQI CDTFMSQGI SCVPESSFMVGGTSLSI SQLCPSSERAFEPASSFQNQLESOM
PGSI SQI CDTFMSQGI SCVPESSFMVGGTSLSI SQLCPSSERAFEPASSFQNGLSSAL
PGLYSGGI KNIDSCKNIDSCKNEHVODTWRELRQCH PVLPCDMINNESVSGALKR VSRVSD
SVNALEDGKKNNDSCKNEHVODTWRELRQCH PVLPCDMINNESVSGALKR VSRVSD
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AKETPRSVALEAPAPLLRVDBWEPARPDVRKASGEGGIKGVRPPPVVLKPPPSWVRPA
VCVVESTWDILRSFAPEDSHAHAPARSGGGDSACQBEEDDDAAAVLTLEELRLGE
TSEEFTGTSSLSTTNDDETSSTTTEAPASRSGGDSACQBEEDDDAAAVLTLEELRLGE
TSEEFTGTSSLSTTNDDETSSTTTEAPASRSGBRFYRAKIRSWRRGMLLGSGSBFGTVF
EGISDEGVFFAVKEVCLCDQGSNAQQCIFQLEQEIALLSQFEHENIVQYYGTDKEDSK
LYIFLELVTQGSLASLYQKYRLRDTHVSAYTRQILNGLTYLHERNIVHRDIKCANILV
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="putative MITE, 51474. .51836
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ATDDGFVDFLQELLFSGTTTTSLGKFVSSGISCGDGSGNISHVKYPTSCISKRRERQA
RLREVLLPVVPPKLSQSLRGPAFVDYLSSMSQISQLENMQLSECKASSKQRRCRQPRH
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41678. .41760,42229. .42259,42907. .43088,43694. .43753,
44229. .44426,44622. .44676,45877. .45992,46149. .46313,
46447. .46620,47271. .47470,47915. .48019,48200. .48263,
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EMLTRQLPYPGLEWTQALYRIGKGEPPAIPNCLSRDARDFISQCVKPNPQDRPSAAKL
LEHPFVNRSMRSIRSMRTSSRSNSSILVLLIMWSWPGRTIRYREAILSTAQSSTPTIA
                                                                                                                                                                                                                                                                                                                                                                                   /note="putative MITE, Cas complement (59793. .62196)
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/note="h.......
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/db_xref="GI:29893594"
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   BX950854
BX950854.12 GI:58190604
HTG:
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
Clade, Panicoideae, Andropogoneae, Zea.
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/mol_type="unassigned DNA"
/db_xref="taxon:4577"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish DUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be
                                                                            · 135 ACACGCACATATGTTTCCTGAA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were atthe Admit) a translation of the contraction of the contr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk On Jan 25, 2005 this sequence version replaced gi:56368832.
                                                                                                                                                                                                                                                                                                                                              75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and the beginning 'drr' were identified by Rick Waterman (Stephen Johnse lab, WashU). For further information see http://www.sanger.ac.uk/Projecte/D_rerio/fishmask.shtml CH211-125M22 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes; Cyprinidae, Danio.
1 (bases 1 to 171896)
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Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: zfish-help@sanger.ac.uk
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                        ACTCCCACATTTCTCATTTAAA 158463
                                                                                                                                                                                                                                                                              TGGCATACTACATGCTTCATCCATCCTTCCATCCATCCAAGCCTTGCCTATT 74
                                                                                                                                                                                CTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAA 134
                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon.7955"
/clone="CH211-125M22"
/clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Pred. No. 3.1;
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ORGANISM
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AC104134
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                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (30-APR-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston,R.H.
Direct Submission
Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (04-DEC-2001) Genome
University School of Medicine,
           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:11-8. The clone may be obtained either from the construction of bacterial artificial chromosome libraries.
                                                                                                                                                                                                   Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAPPING INFORMATION:
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Submitted (20-MAR-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                           SOURCE INFORMATION:
                                                                                                                                                                                   http://genome.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0525L16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://genome.wustl.edu
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                                                                                      Frengen, E.,
from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coworkers at http://www.chori.org
TOR: pBACe3.6
/translation="VFGNKMIIPSLDGALFQWDQDRESMETVPFTVESLLESSYKFGD
DVVLVGGKSLTTYGLSAYSGKWYIGALFQWDQDRESMETVPFTVESLLESSYKFGD
DVVLVGGKSLTTYGLSAYSGKWYIGALFQWDGDBAHQBEDILLLQRTQKTVRAIM
DIVLESGNEKWMFSVGHEFLEYIFDMETTRAFFIESTFKNEWNTEBSKIISDVESGEAIM
DIVLEDEDIYGAARGATENGVYLGMYRGQLYLQSSWRISKKFSSSYKALESVTNENA
IIPLFTIKWKPLIHSPSRTTPVLVGSDEFDKCLSSDKFSHEEYSGALSILQYPSDNGY
YLDYYKRERNKRSTQITVRFLDNPHYNKNIRKKDFVLHWWKEIVATILFCIIATTF
IVRALFHPHPHFHRQKKSSETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPFI
VRALFHPHPHFHRQKKSSETQCQTENKYDSVSGEANDSSWNDIKNSGYISRYLTDFEPFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(67723..67923,68904..68966,72276..72377,
80861..81028,84653..8543,86541..86650,89505..89627,
93417..93529,95828..96048,97969..98091,98748..98888,
100430..100592,100805..101039,103259..103392,
105456...>105650))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(66728. .67923,68904. .68966,72276. .72377,
80861. .81028,8453. .85431,86541. .86590,89505. .89627,
93417. .93529,99628. .96048,97969. .98091,98748. .98888,
100430. .100592,100805. .101039,103259. .103392,
105456. .105650))
                                                                                                                                                                                                                                                                                                                                        /note="Homo sapiens eukaryotic translation initiation factor 2-alpha kinase 3 (EIF2AK3), mRNA.; H_NH0525L16. This gene was based on gi(21361154) Continued from H_NH0450E09.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="CpG_island (%GC=66.5, o/e=0.76, complement(66728. .105650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIVKVPILNRWGPLMPFYQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAQLRDKEFYRPI PNPNPKLTDGYPA FKRPHMTAKDLGLPGFFPSQEHEATREDERKF
TSTCHFTYPASHDLHLAQGDPNQVLQSADFPCLVDPKHQPAAEMAKGYLLLPGCPCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="CpG_is 13008. .13484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="CpG_island (%GC=62.5, 59905. .60161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tranblation="magykypgqdpydldiyqsshmydyqpyrkhkysrytpqeqakl
daqlrdkefyrpipnpkltdgypafkrphmtakdlglpgffpsqeheatrederkf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This gene was based
                                                                                                                                                                                                                               /protein_id="AAY24331.1"
/db_xref="GI:62988944"
                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="EIF2AK3"
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(FLJ25369), mRNA.; H_NH0525L16.1
|his gene was based on gi(22749356)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="FLJ25369"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin (34638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="GI:62988943"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .44562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     island (%GC=61.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .34769,35622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .35658,36392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .36484,39039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .35658,36392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o/e=0.89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o/e=0.83,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #Срсв=22) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #CpGs=24) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #CpGs=53) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #CpGs=20) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .36484,39039.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87633 TGGGATTACAAGCGTGAGCCACTGTACCTGGCCAACCTATCTTTTTCTTCCTCCTCTTCCA 87692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'aro, S., Kerteuts...
'ardyna, S., Gord, S., Graham, L., Grand-Pletze, N.,
'ardyna, S., Gord, S., Graham, L., Grand-Pletze, N.,
'ardyna, S., Gord, S., Graham, L., Grand-Pletze, N.,
'ardyna, S., Gord, S., Graham, J., Lievine, R.,
'ardyna, S., Horton, L., Hulme, W., Iliev, J., Levine, R.,
'ardyna, J., Karatas, A., Kells, C., Landers, T., Macdonald, P., Major, J.,
Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Weneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Weneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Weneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Weneus, L., Mihova, T.,
Mathews, C., McCarthy, M., Meldrim, J., Weneus, L., McCarthy, M
                                                                                                                                                      Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCCAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70;
                                                             Boguslavkiy, b., Cook, A.,
                                                                                                                                                                                                                                                                                                                                           Iravers,M., Vassille
Graman,D., Young,G., Zainoun,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                  Stojanovic, N., Talamas, J., Tesfaye Travers, M., Vassiliev, H., Viel, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rise, C., Rogov, P., Roman, J., Roy, Seaman, S., Severy, P., Smith, C., S
                                                Diaz,J.S., Dodge,
                                                                                                                                                                                                                                                            Submitted (09-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cook, A., Cooke, P., Del
Faro, S., Ferreira, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Camarata,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l (bases 1 to 214946)
Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC136896 214946 bp DNA 1i
Homo sapiens chromosome 15, clone RP11-86001,
erreira, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC136896.6 GI:29135656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                irren, B., Nusbaum, C., Lander, arna, N., Bastien, V., Bloom, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCTCCAAG 87761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKVDI FSLGLI LFELLYPFSTQMERVRTLTDVRNLKFPPLFTQKYPCEYVMVQDMLSP
SPMERPEAINI I ENAVFEDLDFPGKTVLRQRSRSLSSSGTKHSRQSNNSHSPLPSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTMDDVVKVGDFGLVTAMDQDEEEQTVLTPMPAYARHTGQVGTKLYMSPEQIHGNSYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGNHCANKLTAFKPTSSKSSSEATLSISPPRPTTLSLDLTKNTTEKLQPSSPKVYLYI
MQLCRKENLKDWNNGRCTIEERERSVCLHIFLQIAEAVEFLHSKGLMHRDLKPSNIF
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                                                                                                                                                                                                                                      to 214946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chang, J., Chazaro, B., Choepel, Y., Collymo
ke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
reira, P., FitzGerald, M., Gage, D., Galagan,
FitzGerald, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.0%;
                              Boukhgalter,B., Camarata,J., Chang,J., Choepel,yook,A., Cooke,P., Corum,B., DeArellano,K., ook,B., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34.6; DI
Pred. No. 3.6;
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Lander,E.
me 15, clone RP11-86001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lander, E., Ali, A., Allen, N., Anderson Bloom, T., Boguslavkiy, L., Boukhgalter, Chazaro, B., Choepel, Y., Collymore, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ., Roy,A., Schauer,S., Schupback,R.,
h,C., Spencer,B., Stange-Thomann,N.,
Tesfaye,S., Theodore,J., Topham,K.,
    Gage, D., Galagan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                       Vo, A., Wilson, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 110127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                                   Zimmer,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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eil,D., Oliver,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete sequence.
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    Gardyna, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI 21-MAR-2003
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                                                                                                                   Choepel, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dodge, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps.
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REFERENCE AUTHORS

DEFINITION ACCESSION RESULT 14 AC136896

SOURCE ORGANISM KEYWORDS /ERSION FOCUS

REFEREN

AUTHORS

REFERENCE AUTHORS

note="single clone coverage"

TITLE JOURNAL

FEATURES

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REFERENCE
AUTHORS
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Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Abouelleil,A., Chang,J., Choepel,Y., Bouslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collywore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Perceira B.
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Center clone name: 860_0
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/rpt_family="HAL1"
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Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
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Mihova, T., Mlenga, V., Murph
O'Connor, T., O'Donn
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Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 141058 bases at least Q40
Consensus quality: 141224 bases at least Q30
Consensus quality: 141289 bases at least Q20
Insert size: 141354; sum-of-contigs
Insert size: 151354; sum-of-contigs
Quality coverage: 8.68x in Q20 bases; sum-of-contigs
Quality coverage: 8.68x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pieces.
CR847532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-JAN-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquirites: clonerequeste.ac.uk Clone requestes: clonerequest@sanger.ac.uk On Jan 15, 2005 this sequence version replaced gi:56309949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR847532.4 GI:57863691
HTG; HTGS PHASEL; HTGS ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
Danio rerio
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CR847532 141554 bp DNI
Danio rerio clone DKEYP-86C9, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Center project name: zKp86C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pelan,S.
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCAACATACTAAGAAAAGAAGGTAGCTTTCTTAACCCAATAAATGTAACCTATGAAAA 35864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MLT1D" 36941. .37015
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36696. .36751
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Pred. No. 4.2;
D; Mismatches
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DRAFT SEQUENCE, 3 unordered
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Search completed: March 5, 2006, 21:55:32 Job time: 690.29 secs
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                                                                                          90342 TCAAAAAAAACTTATTAGTCC 90362
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                                                                                                                               132 CAAACACGCACATATGTTTCC 152
                                                                                                                                                                                                               72 ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                          12 ACATGCCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
/mol_type="genonic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-86C9"
/clone lib="DanioKeypilot"
1. 10378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:00621.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:00017"
10479. .42327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="assembly_fragment:00290"
12428. .141554
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10478: gap of 100 bp
42327: contig of 31849 bp in length
42427: gap of 100 bp
41554, contig of 99127 bp in length.
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	AAF15843	ADB92108	ADB96917	ADB87934	ADB20845	ACF62730	ABD32806_5	ACN45162	ADX13304	ADX11599	ABN67847	ADW26566	ADD71973	AAS32893	AAS32892	ADS57339	ADA68284	AAT42063_06.	AAL62902 .	AAF22303 2	ADF00796	AAH13328	ADD33404	ADD33403	AAH76335	ADB12064 07
	Aaf15843 Human pro	Adb92108 Human MDR	Adb96917 Human MDR	Adb87934 Human UGT	Adb20845 MRP1 base	Acf62730 Cancer ba	tion (Acn45162 Human gen	Adx13304 Plant ful	<pre>Adx11599 Plant ful</pre>	Abn67847 Streptoco	Adw26566 Glycine m	Add71973 Human uri	Aas32893 Human gen	Aas32892 Human gen	Ads57339 Bacterial	Ada68284 Arabidops	Continuation (7 of	Aal62902 Vernonia	Continuation (3 of	Adf00796 Bacterial	Aah13328 Human cDN	Add33404 Mouse mit	Add33403 Mouse mit	Aah76335 Z. mays M	Continuation (8 of

ALIGNMENTS

	CC promoter operably linked to (1) into a plant where the exogenous gene CC impacts male fertility of the plant and (1) controls expression of the CC exogenous gene. A method of producing hybrid seeds is also provided. The	the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a	The invention provides a male tissue-preficomprising nucleotide sequences essential	PS Example 5; Fig 8; 50pp; English.	fertility in a male plant.	A male tissue-preferred regulatory region comprising essential for initiating transcription of the MS45	WPI; 2	PI Albertsen MC, Fox TW, Garnaat CW, Huffman G, Kendall TL; XX	PA (PION-) PIONEER HI-BRED INT INC.	PR 15-FEB-2000; 2000US-00504487. XX	TY 13-FEB-2001; 2001WO-US004527.	PD 23-AUG-2001.	PN WO200160997-A2. XX	OS Zea mays.	XW Ms45; male tissue; regulatory region; transcription; male fertility; XW hybrid seed; promoter; ds. XX	DB Z. mays Ms45 promoter fragment.	DT 29-OCT-2001 (first entry)	XX AAH76340;	RESULT 1 AA176340 ID AA176340 standard; DNA; 255 BP.	
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RESULT 2
AAX07408
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                                                                                                     The sequence is that encoding an Ms45 male tissue-preferred regulatory region. It may be used in the construction of a vector for a method of producing exogenous genes in a male tissue- preferred manner, which is useful in restoring or conferring ferrility, such as in hybrid seed production. In conferring fertility, a monocot/dicot plant is transformed with the exogenous nucleotide sequence (a male sterility gene, preferably Ms45), which encodes a product selected from auxins, rolls and diptheria coxin. Hybrid seeds are produced by cross-pollinating maize male fertile and infertile plants
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                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                 New nucleic acid encoding
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                                                                                 Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T;
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CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC
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100.0%; F
Live 0;
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Pred. No. 1.4e-42;
                                     Score 157; I
Pred. No. 2.4
D; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory region; plant cells; maize; hybrid seed; fertility;
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2.4e-42;
98 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 23-24; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albertsen MC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                     CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
                                                                           AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
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                                                                                                                  CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCCTTGTTCCATCGTCC
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CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC
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100.0%; Pred. No. 2.4e-42;
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RESULT 5
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Best Local (
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                29-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1394 BP; 411 A; 311 C; 231 G; 441 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from Z. mays
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                                                                                      AAH76333 standard;
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    mays Ms45 male tissue-preferred regulatory region encoding

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                                                                                                                                                                           CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                                                          CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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ilarity 100.0%;
Conservative (
                (first entry)
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                                                                                    DNA;
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Pred. No. 2.4e-42;
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Best Local
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            WO200160997-A2
                                               Zea mays.
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                                                                                                                                                                                                            AAH76334;
                                                                                  hybrid seed; ds.
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157; Conserva
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The invention provides a male tissue-preferred regulatory region (I) comprising nuclectide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a nucleic acid sequence encoding an Ms45 male tissue preferred regulatory region from Z. mays
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                                                                     Z. mays Ms45 male tissue-preferred regulatory region fragment
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Ms45; male tissue; regulatory region; transcription; male fertility;
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ilarity 100.0%;
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Pred. No. 2:4e-42;
Pred. No. 2:4e-42;
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RESULT 7
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Best Local Sim:
Matches 157;
  22-JUN-2001;
24-AUG-2001;
26-SEP-2001;
21-NOV-2001;
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                                                                                                                                                                                                                                                                                                           Oryza sativa
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  ; 2001US-0300112P.
; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                          2002WO-US019668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                        tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 146; DB 5;
Pred. No. 6.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kendall
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Ms45; male tissue; regulatory region; transcription; hybrid seed; ds.

male fertility;

WPI; 2001-514772/56 Albertsen MC, 13-FEB-2001; 2001WO-US004527

15-FEB-2000; 2000US-00504487.

PIONEER HI-BRED INT INC

Fox TW,

Garnaat CW,

Huffman

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23-AUG-2001 WO200160997-A2 **Zea mays** mays Ms45 male tissue-preferred regulatory region fragment

AAH76336;

AAH76336 standard;

DNA;

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29-OCT-2001

(first entry)

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Best Local S
Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acinelecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, sal stress, osmotic stress or any of their combinations. The present sequent is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel abiotic stress responsive polymucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polymucleotides. Also disclosed are methods for using the polymucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2000 BP; 616 A; 370 C; 355 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                 CCTCCATGCA 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 17293; 89pp; English.
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T, Provart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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N, Ricke D,
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D, Zhu T;
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The present sequence
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RESULT 9
AAH76337
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Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the M845 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment -72 to -111 bases upstream of the TATA box of a Z. mays M845 male-tissue preferred regulatory region
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The invention provides a male tissue-preferred regulatory region (I) comprising nucleotide sequences essential for initiating transcription of the MS45 gene. A method of mediating male fertility in a plant is provided that involves introducing an expression vector comprising a promoter operably linked to (I) into a plant where the exogenous gene impacts male fertility of the plant and (I) controls expression of the exogenous gene. A method of producing hybrid seeds is also provided. The present sequence represents a DNA fragment upstream of the TATA box of a Z. mays MS45 male-tissue preferred regulatory region nucleotide sequence
                                                                                                                                                                                                                                                                                                              A male tissue-preferred regulatory region comprising nucleotide sequences essential for initiating transcription of the MS45 gene useful for mediating fertility in a male plant.
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hybrid seed; ds.
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                                                                                                                                                                                                                                                                   Claim 14; Page 32; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PION-) PIONEER HI-BRED INT INC
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50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulatory region; transcription; male fertility;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garnaat CW,
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Pred. No.
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8.1e-07;
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2774 TICTTTTCTCACCICCCICIGATTTCTTTGTACCTCACTTTCATTTTGGCCTTTAAGTT 2833

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Query Match
Best Local Similarity
Matches 66; Conserv

Conservative

0;

56;

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98

20.6%;

Score 32.4; DB pred. No. 2.5; 0; Mismatches

DB

Length 3267; Indels

Sequence 3267 BP; 1029 A; 658

C; 590 G; 990

T; 0 U; 0 Other;

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RESULT 10
ADK52131
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                                The invention relates to detecting atopic dermatitis or psoriasis comprising assaying the levels of expression of an indicator gene at a rash site and non-rash site of a person with atopic dermatitis or psoriasis, comparing these levels with those of a healthy person, and determining that if the levels of indicators are higher or lower then this indicates the disease. Also included are a reagent for detecting atopic dermatitis or psoriasis, a kit for screening for treatments, a transgenic non human vertebrate animal models for the diseases, an agent for inducing the diseases in mice and a DNA chip for assaying for the indicator genes. The method is used for treatment, detection and animal models for research of atopic dermatitis and psoriasis. The present sequence is a Mouse atopic-dermatitis/psoriasis-associated EST
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                                                                                                                                                                                                                                       Detecting atopic dermatitis or psoriasis expression of an indicator gene at a rash person with atopic dermatitis or psoriasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; ss; EST; atopic dermatitis; anti-inflammatory; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse atopic-dermatitis/psoriasis-associated
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                                                                                                                                                                                                                                                                                                                        Mitsuishi
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14-MAY-2003; 2003JP-00136544.
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                                                                                                                                                                                                              Claim 20; SEQ ID NO 164; 484pp; Japanesė.
                                                                                                                                                                                                                                                                                             WPI; 2004-214514/20.
                                                                                                                                                                                                                                                                                                                                     Itoh M,
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                        (expressed sequence tag).
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i K;
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100.0%; Pro-
---tive 0;
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Pred. No.
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RESULT 11
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         CC the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid ce encoding a polypeptide whose expression is inhibited by the antisense comparising the vector; (3) an isolated concluding a polypeptide whose expression is inhibited by the concluder acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular consideration or the activity of a gene in an operon required for consideration; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway consideration, or that inhibits cellular proliferation; (8) compound that influences the activity of a gene or its gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the colliferation of an organism. The antisense nucleic acids required for identifying an ordered for bomologous nucleic acids required.
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06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342923P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 36272; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
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Trawick JD,
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Forsyth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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Xu HH;
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RESULT 12
ABN80329/G
ID ABN803
XX AEN803
XX AEN803
XX Human;
XW Human;
XW Human;
XW Homo E
OS Synthe
YX GWALF!
XX HOZO02
XX AEN80
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Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2352
                                                                                                                                                                                                    Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for cellular proliferation to isolate candidate molecules for radrug discovery programs, or for screening homologous nucleic aci required for proliferation in cells other than S. aureus, S. typ. K. pneumoniae or P. aeruginosa. The present sequence is one of t
                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP007536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human chemically modified disease
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                                                                                                                                                                                                                                                                                                                                EPIGENOMICS
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                                                                                                                                                                                                                                                                                                 Piepenbrock C,
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Pred. No. 4.2;
O; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes;
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing development genes, in particular disease related diseases, syndromes

Claim 1; SEQ ID NO 346; 27pp; English

development genes, in parti genes (HOX), like diabetes, associated with congenital

ce diabetes, cancer, apoptosis related congenital heart disease, epilepsy, di

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RESULT 13
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Query Match
Best Local S
Matches 53
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                                                                                                                                                                                                Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15734 BP; 3630 A; 744 C; 4234 G; 7126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2000; 2000WO-US007392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAC containing repeats from centromeres 1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF22279
                                                   The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors,
                                                                                                                                                                  Claim 102; Page 321-335; 1449pp; English.
                                                                                                                                                                                                                                                                                                                                                    (UYCH-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200055325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Centromere; michrosome; vector; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                              -SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                               -SEP-1999;
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53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                  Copenhaver
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99US-0127409P.
99US-0134770P.
99US-0153584P.
99US-0154603P.
99US-0172493P.
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Pred. No. 9;
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Sequence 64415

BP; 18698

A; 13554 growth

C; 13083 G;

18980

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0 U; 100 Other

Sequence

18256 A; 19684

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20062

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20204

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1261

Other;

antibodies,

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invention also encompasses expression vectors and host cells comprising a CC A nucleic acid, a polypeptide (especially an antibody) that specifically CC binds to the protein, and a biochip comprising an antibody) that specifically CC carandom. Many of these do not carry transduced host oncogenis or pathogenic trans-acting viral genes, meaning that cancer incidence is a CC direct concequence of the effect; of proviral integration into host CC carcinoma (especially breast cancer, proviral integration into host CC carcinoma (especially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular CC therapeutic agents and in screening and evaluating drug candidates. The CC therapeutic agents and in screening and evaluating drug candidates. The CC sequence of the invention. Note: The complete sequence data for this sequence of the invention. Note: The complete sequence data for this CC in electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
ADA02717
ID ADA02
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant nucleic acid encoding carcinoma associated useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                    The invention relates to recombinant carcinoma associated (CA) acid sequences from mouse and human (ADAO1482-ADAO3094), and tracombinant carcinoma associated proteins (CAP) encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1235; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-DEC-2001; 2001US-00035832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse Nfatc1 carcinoma associated
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79467 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC
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19.5%;
Best Local Similarity 56.4%;
Matches 57; Conservative

Score 30.6; Di Pred. No. 28; 0; Mismatches

DB 9;

Length 79467;

44; Indels

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Gaps

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RESULT 15
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                                                                                                        Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                              The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAR-2001; 2001US-00798586.
23-CCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                 Sequence 79467 BP; 18256 A; 19684 C; 20062 G; 20204 T; 0 U; 1261 Other;
                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 283; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                          New recombinant nucleic acid, useful for treating carcinomas, lymphomas, cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-239337/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas; cancer; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2001; 2001WO-US051291.
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                                          53839 CACACACACACACACACACACACACAAGCTTGTGGCTC 53879
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                                                                       TCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCAT 110
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Engelhard EK;
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                                                                                                    19.5%; Score 30.6; D
56.4%; Pred. No. 28;
tive 0; Mismatches
                                                                                                                                   DB 10; Length 79467;
                                                                                                        44; Indels
                                                                                                   0;
                                                                                                    Gaps
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53839 CACACACACACACACACACACACACAAGCTTGTGGCTC 53879

'n 2006, 18:11:35

Search completed: March Job time: 107.48 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                a
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .41078325 seqs, 23393541228 residues
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157
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yb_gss1:*
gb_gr
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                  Length DB ID
                                              0 CG224225

0 CW324513

0 CW324514

0 CW445575

0 CO689491

0 CZ727957

0 DB505306

0 CW871670

0 CW471670

0 CW49746438

0 CW5974281

0 CW599444
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CC656939 OGMDQ20TV
CC252932 CGMDQ20TM
CC656933 CGMDQ20TM
CC656933 CGMDQ20TM
CC656935 CGMDQ20TM
CC7324514 104 819 1
CC6588104 tigr-9ss
CC689495 DC11-25n6
AG366773 Mus muscu
CC727957 OC Ba005
BB505306 BB505306
CC8727957 OS BE263-4
CL026582 CH216-23G
AI744861 Et16b06-23G
AI744861 Et16b06-23G
AI744861 JGI_XZG22
CC558661 OA ABa013
CC442481 JGI_XZG24
CC558661 OA ABa013
CC442481 JGI_XZG64
CC559142 OA ABa013
CC459142 OA ABa013
CC499444 OA ABa013
CC404657 DC680Phil
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1 CGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCC 60

Query Match Best Local Matches 15	FEATURES SOURCE		RESULT 1 CC656939/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE OCCANION		
/ Match 100.0%; Score 157; DB 9; Length 687; Local Similarity 100.0%; Pred. No. 2.2e-39; 1es 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Fax: 301-838 Email: whites Seq primer: Class: methy for	Eukaryota; V Spermacophyt clade; Panica 1 (bases 1 Whitelaw, C.A Resnick, A., Comsortium (Comsortium (SSS) Contact: Cata TIGR 9712 Medical	CCG CCGG CCGG CCGG	2.4 20.6 498 2 BE632212 2.4 20.6 500 2 BF225639 2.4 20.6 520 2 BF225639 2.4 20.6 527 2 BE448824 2.4 20.6 528 7 CNA43061 2.4 20.6 539 5 BX528623 2.4 20.6 543 1 AA673664 2.4 20.6 542 1 AA673664 2.4 20.6 542 2 BF020472 2.4 20.6 543 2 BF133867 2.4 20.6 545 2 BF020472 2.4 20.6 547 5 BX517541 2.4 20.6 570 2 BE114144 2.0 6 570 2 BE114144 2.0 6 571 1 BB004373 2.4 20.6 621 1 BB004373 2.4 20.6 621 1 BB004373 2.4 20.6 621 1 CNS004Y 2.4 20.6 621 1 CNS006YY 2.4 20.6 621 1 BB004373 2.4 20.6 621 1 BB0048833 2.4 20.6 621 1 BB0048833 2.4 20.6 859 10 CNS006YY 2.4 20.6 859 10 CNS0551A 2.4 20.6 1039 11 CNS0551A 2.4 20.6 1039 11 CNS0551A 2.4 20.6 2194 4 BC048853 2.4 20.6 2194 4 BC048	2.4 20.6 347 2 BE690384 BE690384 uw66f12. 2.4 20.6 483 1 AJ746802 AJ746802 AJ746802 2.4 20.6 497 1 AW990724 AW990724 uf10b11.

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  CC656933 963 bp DNA linear GSS 19-UT OGWDQ20TM ZM_0.7_1.5_KB Zea mays genomic clone ZMWBMa0554D15.
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1 (bases 1 to 915)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Whitelaw,C.A., Gusckenbush,J., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
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CG224225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
Fax: 301-838-0208
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Other_GSSs: OG1AG08TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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/clone = Ib="ZM_0.7_1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII;
methylation filtered genomic DNA librar
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/strain="B73"
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CW324514.1
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Renick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWDQ20TV
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 702)
1 (bases 1 to 702)
1 (bases 1, Nunberg, A., Citek, R.W., Robbins, D., Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D., Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., McMenamy, J., Smith, M., Holeman, H., Roe, B.A, Wiley, G., Korf, I.F., Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
                                                                                                                                                                                                                                                                                                         CW324514 702 bp DNA linear GSS 31-OCT-2004 104 819_11477203_148_35910_078 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11477203, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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CC656933
CC656933.1 GI:32060225
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Sorghum bicolor
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Class: methylat
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    Martienssen, R.A.
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/strain="B73"
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                                    Contact: Bedell JA
Orion Genomics, LLC
4041 Forest Park Ave, 9
Tel: 314 615 6979
Fax: 314 615 5975
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Sorghum bicolor (sorghum)
Sorghum bicolor (sorghum)
Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD:
clade; Panicoideae; Andropogoneae; Sorghum.

[ (bases 1 to 296)
Bedell, J.A., Budiman, M.A., Numberg, A., Citek, R.W., Robbins, D.,
Jones, J., Flick, E., Roblifing, T., Fries, J., Bradford, K.,
McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.F.,
Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and
Martienssen, R.A.
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Sorghum bicolor genomic c
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Seq primer: SWfor Forward
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11 Forest Park Ave,
: 314 615 6979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s: methylation filtered
quality sequence stop: 702:
Location/Qualifiers
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                                                                                                                                                 num genome sequencing by methylation filtration Biol. 3 (1), e13 (2005)
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jbedell@oriongenomics.com
fsbb001f170 row: m column: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="organ: leaf, Vector: pBCSK(-), Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 8 the fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
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mol_type="genomic DNA"
cultivar="ATx623"
db_xref="taxon:4558"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      column: 19
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Pred. No. 3.9e-09;
D; Mismatches 5;
                                                                             St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 bp DNA linear GSS 02-NO methylation filtered library (LibID clone fsbb001f170m16, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation filtration
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                                                                               MO 63108, USA
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CE588104/c
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Class: methylation filtered
High quality sequence stop: '
Location/Qualifiers
                                                                                                                                                                                                                                                                        Contact: Kirkness EP
The Institute for Genomic Research
Department of Eukaryotic Genomics, T.
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281
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tigr-gss-dog-17000366359543 L
genomic survey sequence.
CE588104
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

    (bases 1 to 636)
    Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

                                                                                                                                                                                                                                                                                                                                                                                                                The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CE588104.1 GI:36904885
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                                                           /organism="Canis familiaris"
/mol types "genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/clone llb="Dog Library"
/note="Stet e : BstXI; Libraries wiperipheral Elood"
                                                                                                                                                                                                                                                            ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."
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/mol_type="genomic DNA"
/cultivar="ATx623"
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      24.1%;
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Pred. No. 0.00042;
         Score 37,8;
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9712 Medical

Center Drive,

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CO689495/c
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AG366773/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       333 TATTTTTTCCCAGTTCAAGGCATCCTTGTTTGGACCCAAGGGTATACCTCATTTTTAAAA
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                                                                                        sequence.
AG366773
AG366773.1
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DG11-25n6 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.
CO689495
                                                                                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schlueter,T., Hermanns,J., Weindel,M.,
Henrich,J. and Loebbert,R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                  Mus musculus molossinus (Japanese wild mouse)
Mus musculus molossinus
                                                                                                                                             AG366773
Mus musculus molossinus
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Schlueter, T., Herma
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Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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/clone_lib="DG11-kidney"
/note="Organ: kidney; Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9615"
/tissue_type="kidney"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain="Beagle"
                                                                                           GI:47977978
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clone:MSMg01-170B12.TJ,
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                    142 CATATGTTTCCTG 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Tel:81-45-503-9111, Fax:81-45-503-9170)

Tolones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, pio Resource Center, Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Oryza coarctata (Porteresia coarctata)
Oryza coarctata
Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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R.Site
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                                                                                                     GSS.
                                                                                                                                        OC_Ba0055L24.f OC_Ba Oryza 5', genomic survey sequence. CZ727957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hattori, M., Toyoda
Direct Submission
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Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing : TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                     CZ727957.1 GI:71136431
                                                                                                                                                                                                    CZ727957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="mixture of kidney and spleen"/clone_Tib="MSMg01 Mouse Male BAC Library"
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: ECORI.
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Pred. No. 0
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Moriwaki, K.
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BOC__Ba0055L24
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REFERENCE
AUTHORS
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                                                                                         1 (bases 1 to 700)

Arakawa, T., Carrinci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura
Konno, M., Okazaki, Y., Okido, T., Saito, R., Tsakai, C.,
Sano, H., Saeski, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T.T., Muramatisu, M., and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55;
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute.
                                                     RIKEN Mouse ESTs
Unpublished (2001)
On Jul 27, 2000 to
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciunognathi; Muroidea; Muridae; Murinae; Mus.
1 (hasea 1 to 700)
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Mammalia; Eutheria;
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BB505306 RIKEN full-length enriched,
female mammary gland Mus musculus cI
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Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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Kim,H., Collura,K., Wissotski,M., Byrne,M., Stum,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., S
                                                                                                                                                                                                                                                                                                                                                                                              BB505306.2 GI:16442791
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036,
                                                                                                                                                                                                                                                                                                                                                       fus musculus (house mouse)
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/lab_host="DH10B"
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                                                     this sequence version replaced gi:9514268.
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ed, 10 days lactation, adult
cDNA clone D730002G06, mRNA
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Soderlund,C.
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Computer - based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of concedundant cDNA library. Genome Res. 11 (2), 281-289 (2001). Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Kanada, I., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Ianaka,I.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Itoh, M., Konno, H., Okazaki, Y., Myramatsu, M., Sugahara, Y., Shibata, K., Normalization and subtraction of cap-trapper-selected CDNs to prepare full-length cDNn libraries for rapid discovery of new years. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
GATACCTACTCCCAAACCATCCTTACTCATGCAACTTCCATGCAAACAACACCCACATAT 146
                                                                                             TTCTTTTTCTCCCCTCCCTCTGATTTCTTTGTACCTCACTTTCATTTTGGCCCTTTAAGTT 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse tissues.
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RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepared and sequenced in Mouse Genome Encycloped
Project of Genome Exploration Research Group in R
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adult female mammary gland"
Inote-"Site 1: Sali, Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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dev_stage="10 days lactation, adult"
lab_host="DH10B"
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                                                                                                                                                                                                                                       Score 34;
Pred. No.
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                                                                                                                                                                                                                                                                     DB 2; Length 700;
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K., Tanaka,T.,
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CW871670/c
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                                                                                                                                                                                            121 CAACT 125
                                                                                                                                                                                                                       178 GAACTACACCACCACAGACACCACAGACACATACACCCCACACACCATTTAACACAGA 119
                                                                                                                                                                                                                                           61 AAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holocephali; Chimaeriformes; Callorhinchidae;
1 (bases 1 to 734)
Venkatesh, B., Tay,A., Dandona,N., Patil,J.G. (
A compact cartilaginous fish model genome
Curr. Biol. 15 (3), R82-R83 (2005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Callorhinchus milii (elephantfish)
Callorhinchus milii
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                 CL026582 1677 bp DNA CH216-23G24_Sp6.1 CH216 Xenopus tropicalis CH216-23G24, genomic survey sequence.
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CW871670
Xenopus tropicalis (western clawed frog) Xenopus tropicalis
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Fax: 65 6779 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 Biopolis Drive, Singapore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular Genetics Lab
Institute of Molecular
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                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Testis"
/clone_Tib="Whole-genome shotgun library of the elephant
shark (aka elephant fish)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Callorhinchus milii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="Male"
                                          GI:40470443
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63 СССТТСССТАТТСТСАЛССАЛСАССАТАССТАСТСССАЛАСЛАТССАТСТТАСТСАТССА
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 1750000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 1677)
Kremitzki,C., Carter,J., McPherson,J., Warren,W.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: Sp6 ATTTAGGTGACACTATAG
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                   AI744861
tr16b06.x1 NCI_CGAP_Ov23
                                                                                                                                                                               Hominidae; Homo.
1 (bases 1 to 440)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Richard K Wilson
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                             Tumor Gene Index
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cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Gen
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    Sequencing
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IMAGE:2218451 3',
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/db_xref="taxon:4532"
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Scoring table:

Title: Perfect score:

Sequence:

OM nucleic -

12088, 13037, 13038, 15039,

15040,

17368, A 17368, A 14091, A 13779, A 17576, A 17576, A 17589, A 17130, A

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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157
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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3680, Ap
4003, Ap
2556, Ap
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
PIONEER HI-BRED INTERNATIONAL, INC.
STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
STREET: Box 1000
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC: compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,499
FILING DATE: CONCURRENTLY HERBHITH
CLASSIFICATION INVERENTLY HERBHITH
CLASSIFICATION NUMBER: 32,733
REPERENCE/DOCKET NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
TELEPONE: SWOHLD INFORMATION:
TELEPONE: (515) 248-4844
INFORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LERGTH: 1394 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-880-499-1
       Query Match
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APPLICANT: Fox, Tim W.
APPLICANT: Carl, Garnaat W.
APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
COMPANY OF THE SECUENCES: 2
                                                                                                                                                         TYPE: nuclei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Application US/08880499 6037523
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US-08-880-499-2
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                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Sweeney, Patricia A.
REGISTRATION NUMBER: 32,733
REFERENCE/DOCKET NUMBER: 0578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Huffman, Gary A.
APPLICANT: Kendall, Timmy L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION
TITLE OF INVENTION: AND METHOD OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/880,499 FILING DATE: CONCURRENTLY HEREWITH CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Johnston
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                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                      single
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PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2070-09-08
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DA
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
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APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1081
LENGTH: 1185
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Best Local
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                                                                                  Matches
                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITITE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR BELING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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LOCATION: (1)...(385136)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human FEATURE:
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o. 6812339
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    35 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA 94
                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                  Conservative
                                                                                                                   18.9%;
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                                                                              Score 29.6; DB Pred. No. 3.4; 0; Mismatches
                                                                              0,
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Pred. No. 14;
0; Mismatches 41; Indels 0;
                                                                                                                                                        DB 3;
                                                                                  34;
                                                                                                                                                            Length 1185;
                                                                                      Indels
                                                                                  0
                                                                              Gaps
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940 CAACAATTTGTTTTTGTCCACCAGAAAGACCTAACCCATTTTCTCCCCAAGGACATATCTA 881

Carlotte Carlotte

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TYPE: nucleic acid
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STRANDEDNESS: double
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TOPOLOGY: Linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1
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US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Query Match 18.6
Best Local Similarity 51.5
Matches 67; Conservative
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SEQUENCE CHARACTERISTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marke
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                      677275 ACTITAAATTCAGCCTGCTTGCTTGCTATTGCATTTGCATTAAATGCAAGCATAGCCT 677216
                                                                                                                                                                                         677215
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2
                                                                                                                                                   132
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                                                                                                                                                                                                                                72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCCCAAACAATCCATCTTACTCA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                            CAACCAACCA 677146
                                                                                                                                              CAAACACGCA 141
                                                                                                                                                                                         ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/557,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rockville
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Dell Pentium
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                                                                                                                                                                                                                                                                                                                                                 Score 29.2; DE Pred. No. 63; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                       Length 1830121;
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SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-643-990A-1
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                                                                                                                             RESULT 7
US-10-158-865-1/c
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GENERAL INFORMATION:
APPLICANT: Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 18.6%; Score 29.2; DB 3; Length 1 Best Local Similarity 51.5%; Pred. No. 63; Matches 67; Conservative 0; Mismatches 63; Indels
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragn |
Patent No. 6846651
                                                                             Sequence 1, Application US/10158865
Patent No. 6846651
                                                              GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                       677275 ACTITARATTICAGCCTGCTTGCTTGCTATTGCATTTGCATTARATGCAAGCATAGCCT 677216
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CURRENT APPLICATION NUMBER: US/09/643,990A
APPLICATION NUMBER: US/09/643,990A
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2
COMPUTER: Dell Pen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186P1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                          132 CAAACACGCA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT 71
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STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Dell Per
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1830121 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamilton O. Smith J. Craig Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Owen White
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Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 1830121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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SOFTWARE: PatentIn version 3.1 SEQ ID NO 1 PRIOR APPLICATION NUMBER: US 09/557,884
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US 08/476,102
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-21
PRIOR APPLICATION NUMBER: US 08/426,787
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1 TITLE OF INVENTION: Thereof, and Uses Thereof FILE REFERENCE: PB186P2C1D1 CURRENT APPLICATION NUMBER: US/10/158,865 CURRENT FILING DATE: 2002-06-03 FEATURE:
NAME/KEY: misc_feature
LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,t,c, TYPE: DNA
ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc feature
LOCATION: (4747)..(4747) NAME/KEY: misc feature LOCATION: (45732)..(45732) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44975)...(44975) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44905)...(44905) OTHER_INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44416)..(44416) OTHER_INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (40808)..(40810) OTHER INFORMATION: n equal NAME/KEY: misc feature LOCATION: (36636)..(36636) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (36543)...(36543) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (29298)..(29298) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (10150)...(10150) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (9921)..(9921) OCHER INFORMATION: n equ OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (45593)..(45593) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36551)..(36 OTHER INFORMATION: n ENGTH: 1830121 ..(36551) n equals equals equals a,t, a,t, a,t, a,t, a,t, a,t, a,t,c, a,t,c, a,t,c, a,t, a) a,t,c, a,t,c, ò ò ò ò ò ò ò ò or g õ 8 ç õ or 9 õ 유 õ ç õ Or. õ ω ú ω ω ω ω ω ω ω ω ω ω ω

NAME/KEY: misc feature LOCATION: (121344)...(121344) OTHER INFORMATION: n equals : FEATURE: FEATURE:
NAME/KEY:
LOCATION: FEATURE: misc feature NAME/KEY: misc feature 107248)..(107248) FEATURE: NAME/KEY: LOCATION: NAME/KEY: misc_feature LOCATION: (65309)..(65309) OTHER INFORMATION: n equals FEATURE: FEATURE: NAME/KEY: LOCATION: NAME/KEY: misc_feature LOCATION: (122167)...(122167) OTHER INFORMATION: n equals FEATURE: NAME/KEY: NAME/KEY: misc_feature LOCATION: (120038) ... (120038) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (119924)...(119924) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc feature LOCATION: (117136)..(117136) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc_feature LOCATION: (105121)...(105121) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (102696)..(102696) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (65313)...(65313) OTHER_INFORMATION: n equal NAME/KEY: misc_feature LOCATION: (55369)...(55369) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (51602)..(51602) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals a,t,c, NAME/KEY: misc_feature LOCATION: (100091)..(100091) OTHER_INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (80024)..(80024) OTHER_INFORMATION: n equals OTHER INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc_feature (51786)..(51786) misc_feature misc_feature (51805)..(51805) equals a,t, a,t, a,t, a,t, a,t, a,t, a,t, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, a,t,c, ì ò 'n ò Ö ò ò ò ò ò ò ò õ ç õ õ õ õ õ õ õ 얹 8 õ ç õ õ ç မ္ e ŧΩ ω ω ø ιO g ω ω Q ω ω ω ω g ω ω ŧΩ ιΩ

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RESULT 8
US-09-949-016-14712/C
US-09-949-016-14712/Application US/09949016
; Sequence 14712, Application US/09949016
; Patent No. 6812239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (131360)...(131360)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals
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LOCATION: (147197)..(147197)
OTHER_INFORMATION: n equals
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals a,t,c,
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OTHER INFORMATION: n equals a,t,c, or g
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals
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OCATION: (139910)..(139910)
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OCATION: (145171)..(145171)
THER INFORMATION: n equals
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OCATION: (142750)..(142750)
                                                                                                                                                                                                                                          677275 ACTTTAAATTCAGCCTGCTTGCTTGCTCTATTGCATTTGCATTAAATGCAAGCATAGCCT
                                                                                                                                                                        677155 CAACCAACCA 677146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEY: misc_feature
ION: (145058)..(145058)
INFORMATION: n equals a,t,c,
                                                                                                                                                                                            132 CAAACACGCA 141
                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                    12 ACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                     ch 18.6%;
1 Similarity 51.5%;
67; Conservative
                                                                                                                                                                                                                                                                             ATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a,t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a,t,c,
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              ASSOCIATED
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RESULT 10
US-09-949-016-15502
; Sequence 15502, App
; Patent No. 6812339
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US-09-949-016-14712
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US-09-949-016-14713/c
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US-09-949-016-14713
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Best Local S
Matches 45
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SEQ ID NO 14713
LENGTH: 64190
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Best Local Similarity
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Patent No.
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION UNMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION UNMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
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CURRENT FILING DATE: 2000-04-14
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                                                                                                          295 CTCATGTAACAT 284
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                                                                                                                                                                                                          55 TCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTA 114
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.5502, Application US/09949016
6812339
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Pred. No. 27;
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RESULT 11
US-09-949-016-17447
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SEQ ID NO 17447
LENGTH: 41815
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Best Local S
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Patent No. 6812339
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012
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APPLICANT: VENTER, J.
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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TYPE: DNA
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33118 ATGTCACATAGAGACATGCATGTA 33141
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                                         122 AACTTCCATGCAAACACGCACATA 145
                                                                                                                            62 AGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGC 121
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                                                                                       AGACATGCAGATTCACACACATCCGCATAGCTGCTCCTACGGATCCCTGGTCACTCATTC
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63.2%;
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RESULT 12

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FILE REFERENCE: CLOO1307

CURRENT ELLING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 191201
LENGTH: 601
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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5582
                                                                                                                                              5642 CAGGGCCTCTGCCTTCCCCTGCCCCCTGCCCCACCTCACCAGGAGGAAGCCCACGC 5583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 GTCCTGACGTTGCATGCACACRTGCACGCGCACAAACACACACACACTCTCTCTCATT
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                                                                 98 CCAMACANTCCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAA 156
                                                                                                                                                                                                                    38 CCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTC 97
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CCTTGCACACCTGATGCCACATCCGCTTGAGTGGCAGGCGAGTGAAGATGTTGCCCCAAA 5524
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RESULT 14
US-09-949-016-16740
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                                                         ; OTHER INFORMATION: Description of Artificial Sequence; No. 6846621e = ; OTHER INFORMATION: synthetic construct US-09-937-862B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16740
                                                                                                                                                                                                                                                                                                                                                                                                                                  ESULT 15
S-09-937-862B-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1674
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               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                 SOFTWARE: Fa
                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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No. 6846623
                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14952
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                                                                                                                                                                               FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                           ION NUMBER:
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   0; Mismatches
                 Score 27.6;
Pred. No. 1
                              DB 3; Length 927;
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 44; Indels
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53 CATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCT 112

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	611 CTTTTGTGGGCATTACAAACGCGTACTCACATTTTTAT 648	113 TACTCATGCAACTTCCATGCAAACACGCACATATGTTT 150	551 CATCATCAAACCCCTCAATATTCTACACCTATGGAACAGCACCCAGAATTTCGATCC	

*Search completed: March 5, 2006, 22:36:21 Job time: 48.8947 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.

Title:
Perfect score:
Sequence: OM nucleic - nucleic search, using sw model Run on: US-10-713-381-1_COPY_1155_1311 157 March 5, 2006, 23:29:31; Search time 225.751 Seconds (without alignments) 5750.985 Million cell updates/sec The state of the s

Scoring table: IDENTITY_NUC Gapon 10.0 , Gapext 1.0 1 cgtgtcatctcacatggcat.....cgcacatatgtttcctgaac 157

Total number of hits satisfying chosen parameters: Searched: 9793542 seqs, 4134689005 residues

19587084

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications NA_Main:*

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9: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is, derived by analysis of the total score distribution.

SUMMARIES

			ററ റ	Ω	Result
21 22 23	16 17 18 19	12 13 14	10 11	76543	ult No.
29.8 29.8 29.8	30.2 30.2 30.2 30	30.6 30.6 4.0	31.6 31.4 30.8	157 146 50 40 32.2	Score 157 157
19.1 19.0 19.0	19.2 19.2 19.2 19.1 19.1	19.5 19.5 19.4	20.1 20.0 19.6 19.6	100.0 93.0 31.8 25.5 20.5	Query Match 100.0
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US-10-027-632-170626 US-09-783-590-10490 US-09-925-065A-285326	US-09-925-065A-153052 US-10-501-282-2923 US-10-501-282-6651 US-10-713-381-4 US-10-027-632-170626	US-10-027-632-244811 US-10-027-632-244811 US-10-052-482-223 US-10-317-273-11	US-10-282-122A-36272 US-09-925-065A-871704 US-09-925-065A-778732 US-10-437-963-1496	US-10-713-381-2 US-10-713-381-3 US-10-713-381-6 US-10-713-381-6 US-10-674-124A-9081	ID US-10-713-381-9 US-10-713-381-1
Sequence 170626, Sequence 10490, A Sequence 285326,	O		Sequence 36272, A Sequence 871704, Sequence 778732, Sequence 1496, Ap	Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 9081, Ap	Description Sequence 9, Appli Sequence 1, Appli

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		Sequence 222444, Sequence 222445, Sequence 222444, Sequence 222445,	Sequence 1, Appli Sequence 78606, A	Sequence 1, Appli Sequence 1, Appli	Sequence 2154, Ap Sequence 11, Appl	Sequence 254612, Sequence 179264, Sequence 179264,	Sequence 285327, Sequence 285328, Sequence 57018, A Sequence 12385, A Sequence 254612,

ALIGNMENTS

Oy 1 CGTGTCATCTCACATGGCATACTACATGCTTTCCACCGTTCGTT	Query Match 100.0%; Score 157; DB 8; Length 255; Best Local Similarity 100.0%; Pred. No. 2.1e-43; Matches 157; Conservative 0; Mismatches 0; Indels 0; G	US-10-713-381-9 ; Sequence 9, Application US/10713381 ; Publication No. US20040221331A1 ; DEDICAMT NO. US20040221331A1 ; GENERAL INFORMATION: APPLICANT: ALBERTSEN, MARC C. APPLICANT: GANAAT, CARL W. APPLICANT: HUFFMAN, GARY APPLICANT: HUFFMAN, GARY ITILE OF INVENTION: USING SAME FILE REFERENCE: 578R FILE REFERENCE: 578R CURRENT APPLICATION NUMBER: US/10/713,381 CURRENT TILING DATE: 2003-11-14 PRIOR APPLICATION UNMBER: US/04/499 PRIOR APPLICATION NUMBER: 08/880,499 PRIOR APPLICATION NOTHER: 1997-06-23 ; NUMBER OF SEQ ID NOS: 24 \$ SOFTWARE: Patentin Ver. 2.0 \$ SEQ ID NO 9 LENGTH: 255 TYPE: DNA GRANLEM: Zea mays
GTTCCATCGTCC 60 GTTCCATCGTCC 74 GTTCCATCGTCC 72 ATCTTACTCATG 120 ATCTTACTCATG 134); Gaps 0;	METHOD OF

RESULT 2 US-10-713-381-1 ; Sequence 1. Application US/10713381 ; Publication No. US20040221331A1

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; SEQ ID NO 2
; LENGTH: 1394
; TYPE: DNA
; ORGANISM: Zea n
US-10-713-381-2
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SEQ ID NO 1
LENGTH: 1394
TYPE: DNA
ORGANISM: Zea mays
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Publication No. US20040221331A1
GENERAL INFORMATION:
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APPLICANT: ALBERTSEN, MARC
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL
                                                                                                                                                   Matches
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APPLICANT: KENDALL, TIMMY L.
TITLE OP INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OP INVENTION: USING SAME
FILLE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
CRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARY
APPLICANT: KENDALL, TIMMY L.
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: WALE TISSUB-PREFERRED REGULATORY REGION AND METHOD TITLE OF INVENTION: USING SAME
FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
                                                                                                                                                 Local Similarity
les 157; Conserv
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                                                                1215 AAGCCTTGCCTÁTTCTGAACCAÁGAGATÁCCTACTCCCAÁACATCCÁTCTTÁCTCÁTG
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                                                                                                                                              100.0%; Score 157; DB 8; llarity 100.0%; Pred. No. 3.8e-43; Conservative 0; Mismatches 0;
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    LENGTH: 158
    TYPE: DNA
    ORGANISM: Zea mays
    US-10-713-381-3

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) ORGANISM: Zea mays
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                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
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APPLICANT: ALBERTSEN, MARC C.
                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10713381
Publication No. US20040221331A1
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Best Local Similarity
                                                                                                                                                                                                                                            APPLICANT: ALBERTSEN, MARC C.
APPLICANT: FOX, TIMOTHY W.
APPLICANT: GARNAAT, CARL W.
APPLICANT: HUFFMAN, GARL
APPLICANT: KENDALL, TIMMY L.
TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 08/880,499
PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                               FILE REFERENCE: 578R
CURRENT APPLICATION NUMBER: US/10/713,381
CURRENT FILING DATE: 2003-11-14
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TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
TITLE OF INVENTION: USING SAME
                                                                                                                                          PRIOR APPLICATION NUMBER: 08/880,499 PRIOR FILING DATE: 1997-06-23
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                                                                                                                         NUMBER OF SEQ ID NOS: 24
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HUFFMAN, GARY
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Pred. No. 1e-39;
0; Mismatches 0
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Matches

Similarity

DB 8; 5.7e-07

Length 50;

Indels

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PRIOR FILING DATE: 1997-06-23
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                      RIOR APPLICATION NUMBER: PCT/JP00/0762
RIOR FILING DATE: 2000-10-30
RIOR APPLICATION NUMBER: DE2000-112699
RIOR FILING DATE: 2000-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0-674-124A-9081/c
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RRENT FILING DATE: 2003-11-14
OTHER INFORMATION: chr5.fa.07frz.139538206
                                                                                      ID NO 9081
                               GANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           LE OF INVENTION: GENETIC POLYMORPHISM MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6, Application US/10713381 ion No. US200407217777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        9081, Application US/10674124A on No. US20040197797A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AGGATACCTACTCCCAAACAATCCATCTTACTCATGCAAC 124
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40; Conservative
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                                                                                                         SEQ ID NOS: 27110
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                                                                                                                                               CATION NUMBER: JP2002-383869
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0.0014;
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      ORGANISM: Streptococcus mutans
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RESULT 8
US-10-282-122A-36272/c
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Local Similarity 61.2%;
es 52; Conservative
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tion No. US20040029129A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 ATTTTGAAGAAAACAGTGGGCCACCCTCAAAAAAACCCCAAACTACTCATCTAACTTAAAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 AAAAAACCACACATTTGTGATGAA 155
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                                                                                                                                                                                                                                                                                                                                                                      PLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                  RENCE: ELITRA.034A
PPLICATION NUMBER: US/10/282,122A
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen, Kari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Distance between a terminus base of telomere on chromosomal short arm and 5'-terminus of this base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence : 128437212
                                                            2001-02-
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ication data removed - See File Wrapper or PALM
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                                                                                                                 MBER: 60/257,931
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                                                                            60/267,636
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                                       60/269,308
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0; Mismatches
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APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single

TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108627.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE:
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US-09-925-065A-871704
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US-09-925-065A-871704
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR FILING DATE: 2001-08-08
PRIOR PELICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
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Pred. No. 4.9;
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2352;
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PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 778732
LENGTH: 601
TYPE: DNA
ORGANISM: Homo Bapiens
US-09-925-065A-778732
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US-10-437-963-1496/c
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                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1496
LENGTH: 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1496, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                    Matches
                                                                                                                                                 Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 CAAACACGCA 141
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                                                                   234 AÁCÁCTGAĆÁ 225
                               120 GCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 157
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                                                                                                 60 CAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCAT 119
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Zhou, Yihua
Cao, Yongwei
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TCAGATCCACAAATCGCACCCTCCCATATCTGCTGAAC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu, Wei
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Barbazuk, Brad
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                                                                                                                                    Conservative
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                                                                                                                                                  19.6%;
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                                                                                                                                 Score 30.8; DI
Pred. No. 7;
0; Mismatches
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Pred. No. 5.5;
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                                                                                                                                                                  DB 7; Length 1122;
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RESULT 12 US-10-027-632-244811 ; Sequence 244811, Application US/10027632

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RESULT 13
US-10-027-632-244811
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; ORGANISM: Human
US-10-027-632-244811
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                         PRIOR FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE OF INVENTION: Identification and Mapping of Single Nucleotide (TLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION: Identification and Mapping of Single Nucleotide TLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                             REFERENCE: 108827.1
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APPLICATION NUMBER: US 60/198,676
FILING DATE: 2000-04-20
FILING DATE: 2000-04-20
                                                                                APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24 APPLICATION NUMBER: US 60/167,363
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PELICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 GAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTCCATGCAAACACGCACA 143
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CATION NUMBER: US 60/146,002
                                        CATION NUMBER: US 60/156,358
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                                                                                                                                                                     2000-04-20
NUMBER: US 60/193,483
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Pred. No. 6.3;
0; Mismatches
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US-10-027-632-244811
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SEQ ID NO 244811
LENGTH: 559
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 223, Applic Publication No. US20 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/052,482
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Engelhard, Eric
APPLICANT: Morris, David
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RITLE OF INVENTION: NOVEL COMPOSITIONS AND
FILE REFERENCE: A-71087/RMS/DCF
LOCATION: (46579)...(46772)
OTHER INFORMATION: "n" at positoins
                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (10089). (10620)
OTHER INFORMATION: "n" at positions 10089 to 10620 can be any base
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: "n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                           NAME/KEY: misc_feature
LCCATION: (20762) ..(20781)
OTHER INFORMATION: "n" at positions 20762 to 20781 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (4099)..(4369)
OTHER INFORMATION: "n" a
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (5502)..(552
                                                                          OCATION: (30751)..(30916)
OTHER INFORMATION: "n" at positions
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (13273)..(13370)
DTHER INFORMATION: "n" at
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                     KEY: misc_feature
ION: (46579)..(46
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o. US20040072264A1
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                                                                                                                                                                                                                              at positions 13273 to 13370 can be any base
                                                                                                                                                                                                                                                                                                                                                                                at positions 5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                            at positions 4099 to 4369 can be any base
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                                                                              30916 can
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, NAME/KEY: misc feature
, LOCATION: (77382)..(77401)
; OTHER INFORMATION: "n" at positions 77372 to 77401 can be any base US-10-052-482-223
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US-10-317-273-11
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publication No. US20040110158A1
GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Tamara Balac Sipes
TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL RIBOSOMAL PROTEIN L13 EXPRESSION
FILE REFERENCE: RTS-0478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.5%;
Best Local Similarity 56.4%;
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/317,273
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 159
SEQ ID NO 11
                                                                                                                                                                            Matches
                                                                                                                                                                                                    Query Match 19.4%; Score 30.4; Best Local Similarity 61.2%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: 11121, 11122, 11123, 11124, 11125,
LOCATION: 11130, 11131, 11132, 11133, 11134,
LOCATION: 11138, 11139, 11140, 11141, 11142,
LOCATION: 11146, 11147, 11148, 11149, 11150,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 11220
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature

LOCATION: 11187, 11188, 11189, 11190, 11191, 11192, 11193, 11194, 11195,

LOCATION: 11196, 11197, 11198, 11199, 11200, 11201, 11202, 11203,

LOCATION: 11204, 11205, 11206, 11207, 11208, 11209, 11210, 11211,

LOCATION: 11212, 11213, 11214, 11215, 11216, 11217, 11218, 11219

OTHER INFORMATION: n = A,T,C or G

FEATURE:
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LOCATION: 11154, 11155, 11156, 11157, 11158, 11159, 11160, 11161,

LOCATION: 11163, 11164, 11165, 11166, 11167, 11168, 11169, 11170,

LOCATION: 11171, 11172, 11173, 11174, 11175, 11176, 11177, 11178,

LOCATION: 11179, 11180, 11181, 11182, 11183, 11184, 11185, 11186,

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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                          110 TCTTACTCATGCAACTTCCA 129
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                                                                                                                      50 TTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCA 109
                                                                                                                                                                                    49;
TCTTTCTCAGCAAACTTCTA 20134
                                                                                                                                                                                 Conservative
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                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                               31; Indels
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11137,
11145,
11153
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Search completed: March 6, 2006, 03:55:07 Job time: 227.751 secs

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OM nucleic - nucleic search, using sw model
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
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1. /cgn2 6/ptodata/2/pubpna/US06

2. /cgn2 6/ptodata/2/pubpna/US06

3. /cgn2 6/ptodata/2/pubpna/US07

4. /cgn2 6/ptodata/2/pubpna/US09

6. /cgn2 6/ptodata/2/pubpna/US09

7. /cgn2 6/ptodata/2/pubpna/US09

7. /cgn2 6/ptodata/2/pubpna/US10

9. /cgn2 6/ptodata/2/pubpna/US10

9. /cgn2 6/ptodata/2/pubpna/US11

10. /cgn2 6/ptodata/2/pubpna/US1

11. /cgn2 6/ptodata/2/pubpna/US1

11. /cgn2 6/ptodata/2/pubpna/US1

11. /cgn2 6/ptodata/2/pubpna/US1

11. /cgn2 6/ptodata/2/pubpna/US1

12. /cgn2 6/ptodata/2/pubpna/US1

13. /cgn2 6/ptodata/2/pubpna/US1
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Gapop 10.0 , Gapext 1.0
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157
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Match Length DB ID
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2 6/ptcdata/2/pubpna/US10_NEW_PUB.seq: *

/cgn2 6/ptcdata/2/pubpna/US11_NEW_PUB.seq: *

/cgn2 6/ptcdata/2/pubpna/US10_NEW_PUB.seq: *
6 US-09-925-065A-871704
6 US-09-925-065A-778732
12 US-11-117-187-185
12 US-11-121-086-13
13 US-11-121-086-13
14 US-09-925-065A-285326
6 US-09-925-065A-285327
6 US-09-925-065A-285328
6 US-09-925-065A-285328
6 US-09-925-065A-285328
6 US-09-925-065A-285328
6 US-09-925-065A-285328
6 US-09-925-065A-3385
6 US-09-925-065A-33976
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                                                                                                                                         Sequence 871704,
Sequence 778732,
Sequence 1185, Appl
Sequence 113, Appl
Sequence 153052,
Sequence 285326,
Sequence 285327,
Sequence 285328,
Sequence 12385, A
Sequence 12385, A
Sequence 47517, A
Sequence 47517, A
Sequence 47517, A
Sequence 47517, A
Sequence 33976, A
Sequence 33976, A
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. :	e 95915,	e 68127,	e 551/8,	e 551/8,	e 23, App	e 58624,	e 58624,	e 37809,	e 37809,	e 757513,		Sequence 427091,	39884,	39884,		30272,	686354,	68635	8635	Ф	Φ	Sequence 553735,	e 33979,	e 339/8,	· n · ω	

ALIGNMENTS

₽ Q	유 성	Query M Best Lo Matches	; ORC	; SEQ :	NUMBE	PRIOR	PRIOR	PRIOR	PRIOR	PRIOR	CUR	APPLIO TITLE TITLE	RESULT 1 US-09-925-(; Sequence ; Publicati
64 CCTTGCCTATTCTGAACCAAGAG 86 	4 GICATCTCACATGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAG	Query Match 20.0%; Score 31.4; DB 6; Length 565; Best Local Similarity 60.2%; Pred. No. 2.7; Matches 50; Conservative 1; Mismatches 32; Indels 0; Gaps	115: DKG 10GANISM: Homo sapiens US-09-925-065A-871704	SEQ ID NO 871704 LENGTH: 565	EQ H	COR FILING PATE: 2001-01-10 COR STITUS PATE: 2001-05-09 COR STITUS PATE: 2001-05-09	APPLICATION 1	APPLICATION 1	APPLICATION I	≃ ≥	CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08	APPLICANT: Wang, David G. APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135	RESULT 1 US-09-925-065A-871704 ; Sequence 871704, Application US/09925065A ; Publication No. US20040181048A1
	.G 63	0.											

US-09-925-065A-778732/c

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US-11-117-187-185; Sequence 185; A; Publication No.
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/269,846
PRIOR PRILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
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Matches
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SOFTWARE: FRBESEQ for Windows Version 4.0
SEQ ID NO 778732
LENGTH: 601
  Query Match
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 185
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                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/125,219
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
-09-925-065A-778732
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION
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                                                                     NAME/KEY: modified base
LOCATION: (9960)...(21146)
OTHER INFORMATION: N = A,
                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                               FEATURE:
                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                 ENGTH: 64415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 ATTATAAATGÁTAAATTTTTCTÁTACACÁTACÁGTTTTTCTACCCATATTÁTCTTTCCTA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 ACATAGTACACTTTATTTATTGTTTACTGTTGGTCATTTAGGATATTTATACCCTTCCCT
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b. US20050266560A1
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  Score 30.6;
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  DB 12;
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Length 64415;
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER: OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 153052, Application US Publication No. US20040181048A1 GENERAL INFORMATION:
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                                                          NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 153052
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
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ORGANISM: Homo sapiens
                     TYPE: DNA
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ORGANISM: Homo sapiens
                                           ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                             REFERENCE: 108827.135
                                                                                                                                             APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                   FILING DATE: 2001-01-16
                                                                                                                                                                                      APPLICATION NUMBER: US 60/261,766
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Pred. No. 32;
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Mismatches
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US-09-925-065A-153052
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US-09-925-065A-285326
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Best Local S
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                                                                                                                                                                                                                                                                                                           -09-925-065A-285327
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION UNUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                               FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
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                                                                                                                                                                           TLE OF INVENTION: Identification and Mapping of Single TLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
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FILING DATE: 2000-11-20
APPLICATION NUMBER: US 60/250,092
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L Similarity 60.5%;
49; Conservative
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NG DATE: 2000-10-24
                                        CATION NUMBER: US 60/252,147
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; ORGANISM: Homo sapiens
US-09-925-065A-285327
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                                                      RESULT 9
US-09-925-065A-12385
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LENGTH: 617
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Best Local Similarity
Matches 49; Conserv
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-01-16
Sequence 12385, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   Query Match
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PRIOR APPLICATION NUMBER: US 60/289,846
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PRIOR APPLICATION NUMBER: US 60/250,092
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ITLE OF INVENTION: Identification and Mapping of Single
ITLE OF INVENTION: Nucleotide Polymorphisms in the Hum
                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                              433 TACCTGCACTGAAGTTAAATG 453
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Similarity 60.5%;
19; Conservative
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milarity 60.5%;
Conservative 0
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Pred. No. 9;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                        Score 29.8;
Pred. No. 9
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US-11-117-187-209/c
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                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-209
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                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 209
LENGTH: 611587
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
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PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/531,120 PRIOR FILING DATE: 2000-03-17 PRIOR APPLICATION NUMBER: 60/125,219 PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
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NUMBER OF SEQ ID NOS:
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 212
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TYPE: DNA
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                                           270144 TCTCTCCTGCCAAGCGAATGGATTTGTCATGCATTTGTTGCTAACTGCCGACACAAGCTG 270085
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                                                                                                                              h 18.7%;
Similarity 52.0%;
66; Conservative
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Similarity 50.3%;
GCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTTC 127
                                                                                    TCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTCTTGTTCCATCGTCCAAGCCTT 67
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)S: 957086
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Pred. No. 11;
0; Mismatches
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human G
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2001-01-16
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US-09-925-065A-805392
                                          ; ORGANISM: Bovine US-10-750-185-47517
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 805392
LENGTH: 544
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                                                                                                                SOFTWARE: PatentIN version 3.1
SEQ ID NO 47517
LENGTH: 1370
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Best Local
Query Match
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APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING PILE REFERENCE: MMILLION-2
CIPERENT PARTY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -10-750-185-47517
                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 64922
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                                                                                            TYPE: DNA
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KERR, Richard
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18.3%; Score 28.8;
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 544;
Length 1370;
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RESULT 14
US-09-925-065A-845392
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; ORGANISM: Bovine 19866880570548
US-10-750-623-47517
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SEQ ID NO 47517
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Best Local
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TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
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PRIOR FILING DATE: 2002-12-31
                                                                                                              PRIOR APPLICATION NUMBER: US 60/250,092
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"LE OF INVENTION: Identification and Mapping of Single
LE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
JE REFERENCE: 108827.135
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57; Conservative
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ROSENFELD, David
HOLM, Tom
BATEC
SEQ ID NOS: 957086
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                                                                                       CATION NUMBER: US 60/261,766
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                                    TE: 2001-01-16
ON NUMBER: US 60/289,846
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Pred. No. 2
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US-09-925-065A-845392
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Job time : 164.89 secs
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Best Local Similarity 54.9%;
Matches 56; Conservative
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-09-925-065A-33976
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PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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TIE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TIE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
TIE REPERENCE: 10827.135
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FILING DATE: 2001-05-09
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FILING DATE: 2000-10-24
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54.9%; Pred. No. 34;
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Title: Perfect score: Sequence:

US-10-713-381-1_COPY_1_1311 1311

Run on:

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration

Ltd.

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

11766282

5883141 seqs, 28421725653 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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PC C12N15/82,C12N15/29,C12N9/24,C12N9/22,C12N9/10,C12N9/00 PC
C07K14/34,C12Q1/68,
PC A01H5/00
CC Strandedness: Single;
PH Key
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PD 30-OCT-2001
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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/mol_type="genomic DNA"
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Best Local Similarity
Matches 1311; Conserv
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Patent: JP 2001520523-A 2 30-OCT-2001;
PIONEER HI ERED INTERNATIONAL INC
PN JP 2001520523-A/2
PD 30-OCT-2001
PF 19-JUN-1998 JP 1999504910
PR 23-JUN-1997 US 08/880499
PI MARC C ALBERTSEN, TIMOTHY W FOX, CARL W GARNAAT, GARY A HUFFWAN,
PC CIZN15/82, C1ZN15/29, C1ZN9/24, C1ZN9/22, C1ZN9/10, C1ZN9/00 PC
CC TOPOlogy: Linear;

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JP 2001520523-A/2.
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1 (bases 1 to 1394)

Albertsen, M.C., Fox, T.W., Garnaat, C.W.,
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini
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                                                                                          CTCCATGTTCCACTTCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCAT
  CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCCATCAAGGGCCTTTCGGATGGCCCA
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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661 ATTGTTTTTATATACATTTTCTTCTCTTTACAATAGAGTGATTTTCTTCCGATTTTATAAA		541 CAAGCATATTTCGAAAGAGACAAATTATGTTACAGTTTACAACATCTAAGAGCGACAAA 600	481 CGAAAGCTATCATGTAAIGTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAA 540	421 TCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACT 480	361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420 361 GGGCCTCAGCATAGATTTTCGCTTAGGGCCCAGAAATGCGAGGACCAGCCATGTCTAGTG 420	301 TTATTATTCTTTAGATATTATTTAATTTTTGGAAAATAACAACTTATACTTTTGTGTA 360 	241 CGAGACGTATCGGGTCGTGGTGATCCAGGGGATATATGTCCCCCACAATCGTCACCTATA 300	181 CTGACCGAGGCCCATCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCA 240	121 CTCCATGTTCCACCTCTCCCACCTCGCGTTGCACATTCTTGGATGTCGGTGGTTCCCAT 180	61 CTTCTTCTGCCTTATTACTGACTGAATCGGGGTTACAAAAAACTTCCACGGGTGCATGAT 120	1 CCATGGTGTCTCTATGAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 	y Match 100.0%; Score 1311; DB 6; Length 1394; Local Similarity 100.0%; Pred. No. 7.2e-228; hes 1311; Conservative 0; Mismatches 0; Indels 0; Gaps	AX224394 Sequence 1 from Patent AX224394 AX224394.1 GI:15554636 Zea mays Zea mays Zea mays Zea mays Zea mays Zea mays Albertsen, Viridiplanta Spermatophyta; Magnolic clade; Panicoideae; And Albertsen, M.C., Fox.T. W Male tissue-preferred r Patent WO 0160997-A 1 PIONEER HI-BRED INTERNA LOCATION (Oual) 1 1394 / organism="Team" / org

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100.0%; Score 1311; DB 6; Length 1394; Local Similarity 100.0%; Pred. No. 7.2e-228; hes 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CCATGGTGTCTCTATGAAAAAGATGAGTACAATGTGTCTATATCCGTTTTCTTAGGGTCC 60	rce 11394 /organism="Zea mays" /mol type="unassigned DNA" /db_xref="taxon:4577"	clade; Panicoideae; Andropogoneae; Zea. 1 Albertsen,M.C., Fox,T.W., Garnaat,C.W., Huffman,G. ar Male tissue-preferred regulatory region and method of Patent: WO 0160997-A 2 23-AUC-2001;	zea mays SM Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD	AX224395 ON Sequence 2 from Patent WO0160997. NA AX224395 AX224395.1 GI:15554637		1261 CCATCTTACTCATGCAACTTCCATGCAAACACGCACATATGTTTCCTGAAC 1311	1201 TTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAAT 1260	1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200 1141 GGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTTCAACCGTTCGTC 1200	1081 TGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCA 1140	1021 TTCTCTAGATTAGTAAAAAGGGAGAGAGAGAGAAATCAGTTTTAAGTCATTGTCCC 1080	961 GCCAGCCCCATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTAT 1020 	901 TGCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAAATTAATT	841 TTCAAAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGT 900 	781 TITCTGATTTITTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTT 840	721 ATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATC 780 	
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                                     Male tissue-preferred regulatory region and method Patent: WO 0160997-A 3 23-AUG-2001; PIONEER HI-BRED INTERNATIONAL, INC. (US)
                                                                                                                                         Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                        Sequence 3 from AX224396
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Location/Qualifiers
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/db_xref="taxon:4577"
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                                                                                                                                                                                         Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863105.
                                                                                                                                                                                                                                                                                      9712 Medical Center Dr. Rockville, MD 2080
3 (bases 1 to 188283)
3 (bases 1 to 188283)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M. Schubert, K., SanWiguel, P., Ma, J., Pontaroli, A.C., Rohlfing Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, Quackenbush, J.
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Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
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Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
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Chan,A.P., Pertea,G., Sheng,L., Cheung,F., Lee,D., Koo,H.,
Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M.,
Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T.,
Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. a
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Consortium for Maize Genomics -
Unpublished
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Zea mays strain B73 clone ZMMBBc0196I14, ***
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NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                              Center name: TIGR Seq_lib_id: ZGFX
                                                                                                             Contact: maize@tigr.org
                                                                                                                            Web site: http://www.tigr.org/tdb/tgi/maize/
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C., Rohlfing, T.,
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	gap 154521154620 /estimated_length=unknown	gap 142805142904 /estimated_length=unknown	gap 134045134144 /estimated_length=unknown	/estimated_length=unknown	/estimat	/estimated_length=unknown 123478123577		gap 9867698775	gap 9650296601 /estimated_length=unknown	/estimat	/estimated_lengtn=unknown 4975549854	1352	٦ <u>8</u>	gap 2213422233 /estimated length=unknown	/db_xref="taxon:4577" /clone="ZMMBBc0196I14"	/mol type="genomic DNA" /strain="B73"	source 1. 188283 /organism="Zea mays"	halifiers	45 184423: 24 184523:	173344: gap of unknown leng	06 171605: gap of unknown length	6 167505: gap of unknown length	6 162185: gap of unknown length	7 161076: gap of unknown lengtl 7 162085: contig of 1009 bp in	unknown of 1160	 154521 154620: gap of unknown length 154621 159716: contig of 5096 bp in length 	5 142904: gap of unknown length 5 154520: contig of 11616 bp in	 134045 134144: gap of unknown length 134145 142804: contig of 8660 bp in length 	126564: gap of unknown length	123577: gap of unknown 1 126464: contig of 2887 1	104099: gap of unknown length	98775: gap of unknown length	<pre>2 96601: gap of unknown 2 98675: contig of 2074</pre>	 4 9755 49854: gap of unknown length 4 46647 bp in length 	1 49754: contig of 1449	5 35160: contig of 7096	4 27964: contig 5 28064: gap of	22133: contig of 22133 bp ir 22233: gap of unknown length	* as soon as it is available and the accession number will * be preserved.	is record will be updated with th	
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	Direct Submission	Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,	Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,	Rachupka,A., Ramasamy,U., Raymond,C., Retta,K., Kise,C., Kogov,F., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,	O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,	Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., O'Connor, T., O'Donnell, P.,	Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,	Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,	Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,	Perreira.P., FitzGerald.M., Gage.D., Galagan,J., Gardyna,S.,	Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,	Anderson,M., Arachchi,H.M., Barna,N., Bascien,V., Bloom,i., Boguslavkiv,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,	2 (bases 1 to 18619) Birren, B., Nusbaum, C., Lander, B., Abouelleil, A., Allen, N.,	Unpublished	and Messing, J.	Ciade; Panicoldese; Autopogousac; Aca. 1 (bases 1 to 186199) 1 (bases 1 to 186199) 1 (bases 1 to 186198)	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD	Zea mays Enkaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;	12	AC147602 AC147602.5 GI:51315585	Zea mays clone ZMMBBc0334A01, *** SEQUENCING IN PROGRESS **", o ordered pieces.	p DNA linear HTG 17-AU		O TAGUCCIA 3563/			AAATIAGITTATITTCUCTI AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	110111		s; Cons	5.9%; Score 77.2; DB Similarity 80.5%; Pred. 0.0002		/estimated_length=unknown	/estimated_length=unknown	/estimated_length=unknown	/estimated_length=unknown 171506171605	167406167505	162086 . 162185	160977. 161076	159717159816 /estimated length=unknown	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Qor manually edited. This assembly was performed with Arachne (Genome Res. 2002 12: 177-189; Genome Res. 2003 13: 91-96). All trace files for this project are available at the NCBI trace repository
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Birren, B., Nusbaum, C.
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------ Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?). An exact list of reads used in this assembly are available at http://www.broad.mit.edu/annotation/plants/maize/randomclones.html
provided by the submittue.

provided by the submittue.

This sequence will be replaced
by the finished sequence as soon as it is available and
by the accession number will be preserved.

the accession number will be foreserved.

1 100617: contig of 100617 bp in length

100618 100717: gap of unknown length

100718 104730: contig of 4013 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                              of the gaps between them are based on estimates that have
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                                                                                                                        Submitted (24-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirtles: Cathoridgeshire, Cc. Clone requests clonerequest@sanger.ac.uk Clone repusts clonerequest@sanger.ac.uk on Feb 26, 2005 this sequence version replaced g1:60279457.
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 161616)
                                                                                                                                                                                                                                                                                                       Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                 CR936840 161616 bp
Danio rerio clone DKEY-91021, ***
                    Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
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   Center project
                                                                         Center code: SC
                                                                                        Center: Wellcome Trust Sanger Institute
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/cultivar="B73"
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179937. .180036
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156397. .156496
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l15105. .1<mark>1</mark>5204
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115104: contig of 10274 bp in length
115204: gap of unknown length
156396: contig of 41192 bp in length
156496: gap of unknown length
179336: contig of 23440 bp in length
180036: gap of unknown length
186199: contig of 6163 bp in length.
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name: zK9102
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Pred. No. 0.00023;
0; Mismatches 45; Indels 1;
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SEQUENCING IN PROGRESS ***, 13
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Insert size: 160313; 4.7% error; agarose-fp
Quality coverage: 6.55x in Q20 bases; sum-of-contigs Quality
coverage: 6.56x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-91021"
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                          /note="assembly fragment:00463
fragment chain:1"
79168. .97393
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| ragment_chain:1"
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ragment_chain:1"
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3259. .11860
note="assembly_fragment:00794/
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ragment_chain:1"
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3258: gap of 100 bp
11860: contig of 8602 bp in length
11560: gap of 100 bp
21800: contig of 9840 bp in length
21900: gap of 100 bp
45034: contig of 23134 bp in length
45134: gap of 100 bp
47371: contig of 237 bp in length
47471: gap of 100 bp
47371: contig of 100 bp
660727: contig of 19256 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        816 GTTTCTTTCAAAGAATTTTGATTTTTTCAAAAAAATTAGTTTATTTTTCTCTTTATAAAA 875
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         Baumgart, C.
Direct Submission
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Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 25769)
1 (bases 1 to 25769)
2 (Bichinger, L., Szafranski, K., Pachebat, J., Dear, P., Gloeckner, G., Bichinger, L., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                             Sequence and analysis of Nature 418 (6893), 79-85
                                                                                                                                                                                                                                                                                                                                                AC117267.2 GI:42733680
                                              The Dictyostelium Genome Sequencing Consortium (bases 1 to 25769)
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97494. .103542
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fragment_chain:1"
fragment_chain:1"
158991. 1161616
/note="assembly_fragment:00044.0"
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ragment_chain:1"
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ragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 200; Indels
                                                                                                               chromosome 2 of Dictyostelium discoideum (2002) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    959
                                                                                                                                                                                                                                                                                                                                                                                                                                       INV 21-FEB-2004
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815

FEATURES

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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
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TITLE
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CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostellum/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostellum/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biotechnology, Beuten 3 (bases 1 to 25769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Deutsche Forschungsgemeinschaft (DFG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(2957. 3173,3272. 5583)
/note="GeneID exon Scores (in order 24.88, 254.96 - GSCU_ID dd_00753"
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TDVEMSICLHPTLEINKYDSKQGLSRVVKQFPNVNSLTDLTLLYSSNKRPTEFVQIYP
FQIQIKYTKLDGVRCLRVVSAQLQATPDFNTSTSNANISILAMAFTQQAAKIAQQQEY
MESRLHLKANTKLIRSLCUTUDEQWEEFYNFFULREEMEAPLITCIKNKQQRVEKAATD
DEIQVFYKMKNVHKSFVEGGRKKDISRRKGEAEINKQYYNIKFT"
complement (5711. 6796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĀFFILVRHTPRNITVYKVVMGGGGVGKŠAĪIIQFIQNHFVEEYDPTIEDSYRKQVTIS
GLPPIGGSLNIKKSSSSSSSSSSSSKTCLFNKIFSKKKKQVEQAASBSTIDRIGQI
STNRIBANUSYSMSNIKKEVPLITDDCVYCQCOLVILISRESNILVKTCDDSFTWKCEF
CKYSNSNILLEQGEIPNKDSVEYVLSSPSISSTDGSKREESIIIYCIDVSGSMGITT
EVPSLOSEMVNAKKGVKGASGEBYISKLECVGSITTMIDRISJQYPKKRVLVTFS
DEVMIYTQSNSVDGPYITAGDKLEDPDQLIEIGRSMTYDKLFTASGSSBPLKAKIKKL
EPPQSTALGPALIVSAAIASQKMLSEVVICTDGVPNVGLGAIEDLPLGPAQEFYEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mefptkyvyitsnldkpkewftqSemslitttdtiqksfvnnsg
ssssskgfgeavlldildtagqeeysamrdqyvrtgdcfmivfsidsrssfeevsqlk
qhiervkdrddvpiiivgnkvdlesrrqvsrieadqlarslrvpyietsaktrsniee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSPLGSWTDFKIKQFKKLNDIETILSDVEVNLCSSSNNNNNNNNVDDETLTLLGSGSG
SGSGSSSGTSGAQLSGTGYVINHQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSKFNYLEVIKKFSTISRNNKVYPENIWLNIESTHENCYNNSNYLYNKNNNEYQEYLV
FSKQVIKSFLQNGYNIGIKSSKNTFIKIFENNKDKLFSSLPFFYLKNIAENQEFEDYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
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ILSKSEWFRSLEYSSNKKVIFEVFDGFNHEYIENLDRIIKEFRENKVYGVDFSFSFCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="GeneID exon scores (in order of location ranges):
23.68, 1.54, 15.75, 9.21, -4.75 - GSCJ_ID dd_03387"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join (832. .107) 1896. .2053,2231. .2360))
                         Hypothetical protein"
/protein_id="AAS38627.1"
/db_xref="GI:42733683"
                                                                                                                                                                                                                                                                                                            68.61 - GSCJ
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KNSNHWMMPSLKINQIINDNNNNISNINFVQIQSNSSSLSSSCSTYQSCPIEDEHIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="5836255-5862024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                           product="similar to Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .25769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1070,1237. .1349,1533. .1798,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (in order
                                                                                                                                                                                                                                           falciparum (isolate 3D7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of location ranges):
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/translation="MONLIYOFLIKKEYNQQSFLDCILILSINGLYISYDGLLDYCNN
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TLKNERINGNDGEITTTTTTTTTSRSSTTIMTTTTTTNGVNDRNYLLFRQVWRNIVIK
TQILFHLRLYNIHANKKVFLFPIQLVDYKFKGYLQSWYLNYHDDNDDDADEDSYDSDI
DDDDSYSDGGNCSSSGSSDISDIGSSSNSILSUSSSILBELSWRIFKNSL
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SLDGNWLFKQLKHLQPGHKFQQTIKMGQLPSSLTSLILDFRSYKGVIEIGSIPDSYKT
LDYKRNSCSNQESISRNPIFKGITRLVDPSERNQNIKANDISNNVLTSIHFGEHENS
DIGIKSLPNSIREIKFGRAFDRDIKLCPSSITSIDFGNKFNRLENGTLTSIDFGS
KFNQIIPQGIFIHTKLKSLNFGYHFNQIIPADTLPFTLSLNLGGYNREITVKNDEYD
CYGISNKGGFGSNSSSNFCVGGTNNGLEMLKNTTSIKTTLTLAYFRRKIEVGDLPNSI
ESLNLGYHFNQPIGNNVLFKLLKKLFILNSEFNQNISADGCIPFGLQTIYIRNSNMNF
INSLAPLFITKYINIDLSHLF
JOIN(d6184. . 16199,17272. . . 17613,17707. . . . 19331)
/fote="GenelD exon scores (in order of location ranges):
0.08, 32.32, 227.42 - GSCJ_ID dd_00726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /LTAIN I AL LOI = "MSSTIITPIATTTINNNSSTNGIHNSKTNRTLFKNIKNNIPNS
PNAPIKANSYGIIGNGPNNNNKDRKLNSNDGVNFGKKNILFTSKNSMYSTKHS
SSSSILAKNSYGIIGNGPNNNNKDRKLNSNDGVNFGKKNILFTSKNSMYSTKHS
SSSSILAKNEYDIESIKKELKSMDISTGGISPLSSPLRESSPISTIDLESITATTIK
LITDAFVAASSSSVKYTIDVLLSFKSANTKRPIQIDIVENHQKEIVVPLSLPTTPYN
NNNNNNTNNSSOCHNTANGQKYPIFSPQISPFKIAYAQSSSTKTINNNNNNITF
TKKANSNITTPOSNRNNHYNSNTKSSTKKQNPIPFSLNTATPOQKNTTTTPSKKSTT
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TKNSCSSSGGSSCGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGSSSGGTSGSSSGGTSGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGGTSGGSSSGTTHCPEGYHCGMNNDVATCLASTTGGTGLPGTSSGTAGVSSCLTT
LCPIGHICVEDSNGVNCVPNGGGTSGGSSSTGTSGGHPDPCRDVDCPDGFHCECKDGK
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NTNPCSNVNCPDGFYCEKDGKTAKCVPSDGFPQPFECKDPKGLCPPNHECKFNDQHQ
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VDQHGKECCVVAHRPPPKCSLRCPPPHECRVNHFGEECCVKVHPDKCSLRCPPGHECK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mold). Hypothetical 97.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEEKIKFYFEIIDFQNQKFKIQBFTSKLIGLKESSFTTFKPIVY
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DDYIFEKINSLNMKLNEKEKLINSLIYYNNKGHENKIGFBFMEIINEROFTHKESFQR
IINANSLWIKSIDSRNISNSFINSRCSFNEYFEKRSDASGDFILTIAMIGIMDNYI
ENSIIESKEFQTINYHAKSFFLLINDLYSFMREINBUDLNYIKIATQLNSTQLST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="GeneID exon scores
23.29 - GSCJ_ID dd_00728"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNSMSPPPKLDKRRFSRDLIPFTIANI"
join(8924. .9076,9236. .10573)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLRIQKEQLKQIDDDDDDDDDDDDDDSSPSPPPPPTTTKTFCLSPRPIIKKEENID
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/note="GeneID exon scores (in order of
/.42, 136.56 - GSCU_ID dd_00727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTIELIIDHYLKFLSSIETILKLYQNDQSTYQLLKQVFQNSNKILSGIYFAHKKSKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="AAS38629.1"
/db_xref="GI:42733685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (10972. .11979)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.37, 128.60 - GSCJ_ID dd_00729
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/product="similar to Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cyostelium discoldeum (Slime
kDa protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location ranges):
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RESULT 12
AC155379/c
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Best Local
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Zea mays strain B73 clone
***, 27 unordered pieces.
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Chan, A. P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., Sanwiguel, P., Ma, J., Pontaroll, A.C., Rohlfing, T. Buddiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Is not known and where the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence this record will be updated with the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
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Seq_lib_id: ZOCF
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C., Rohlfing, T.,
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AC155618/c AC155618/c AC155618 AC155618 AC155618 AC155618 AC155618 DEFINITION 2-a mays strain B73 clone ZMMBBc0344D04, *** SEQUENCING IN PROGRESS ***, 21 unordered pieces. ACCESSION AC155618.2 G1:58082477 KEYWORDS Eda mays Eda m	/estimated_length=unknown 1215973146 12159731469 /estimated_length=unknown gap /esti

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be preserved.
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                                                                                                                               organism="Zea mays"

mol_type="genomic DNA"
estimated_length=unknown
10469. .30568
                                              estimated_length=unknown
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Plasmodium falciparum sexual
partial cds.
                                                                                                                                                                                                       AF034389.1 GI:3098290
                               Dechering, K.J., Kaan, A.M., Mbacham, W., Wirth, D.F., Eling, W., Konings, R.N. and Stunnenberg, H.G. to two distinct Isolation and functional characterization of two distinct sexual-stage-specific promoters of the human malaria parasite Plasmodium falciparum
                                                                                                                   Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                    lasmodium falciparum (malaria parasite P. falciparum)
Lasmodium falciparum
                   Cell. Biol. 19 (2), 967-978 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                444 СААБАТТТААЛАЛААТААССАААБТААСТААТССАСТСБАААБСТАТСАТБТААТБТТТА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 713)
Dechering, K.J., Kaan, A.M. and Konings, R.N.H.
Direct Submission
Submitted (12-NOV-1997) Molecular Biology, University of Nijmegen,
Toernooiveld 1, Nijmegen 6525 ED, The Netherlands
                                                                                                                                                                                                                                                                                                                                                                                                                                 AATATTATCCTATGATAATAAAGCTATTGTGGAAATTATATTTTATGGAAAATATAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTTCAGATTTTTCTTTTCATTCTTGTTATTTGTTTTTTTATATACATTTTCTT
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CCGAAACTGAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAGGGA 104
                                                                          TTCCCAATAAATTACAATCACTGTGTATAATTATTTGGCCAGCCCCATAAATTATTTAAA 983
                                                                                                       CTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGACTAGCCCTAGAATGTT
                                                                                                                                                             TTTATTTATTTTATATATATAATTTTTTTTAAATTTTAAATTTCATATATTTTTAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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537. .710
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537. .>713
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/product==sexual_stage_antigen"
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/db_xref="GI:3098291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="816"
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/mol_type="genomic DNA"
/strain="NF54"
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711. .>713
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Pred. No. 0.0063;
0; Mismatches 33
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                            misc_feature
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Dictyostelium discoideum MigA (migA) gene,
U86962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escalante, R., Wessels, D., Soll, D. and Loomis, W.F.
Direct Submission
Submitted (27-JNA-1997) Department of Biology, University of
California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on migA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

(bases I to 3576)

Escalante,R., Wessels,D., Soll,D.R. and Loomis,W.F.

Chemotaxis to CAMP and slug migration in Dictyostelium both depend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum
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Biol. Cell 8 (9),
                                                                                             951. .1289
/gene="migA"
/note="encodes
                                                                                                                                                                                                                                                                                                                                                            /function="essential for slug migration"
/note="N-terminus of this protein is similar to other BTB
domain proteins, such as the Mus musculus and human zinc
finger proteins encoded by GenBank Accession Numbers
/114556 and L16896, respectively"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_strain="AK244"
/db_xref="taxon:44689"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Dictyostelium
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/gene="migA"
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/gene="migA"
                                          /gene="migA"
/number=1
                                                                                     LEIYGELCETNPNPN'
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Best Local Similarity 47.2%; Pred. No. 0.00
Matches 217; Conservative 0; Mismatches
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432 ATTTTTTTTATTTAATTTTATTTTTATTTTATTTTTTT 393
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ceplace="pbsr1 external plasmid, approximately 4 kb".
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Search completed: March 5, 2006, 21:55:27 Job time: 5725.47 secs

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Title: Perfect score: Sequence:

US-10-713-381-1_COPY_1_1311 1311

Run on:

OM nucleic - nucleic search, using sw model

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST:*

gb_est1:*

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

82156650

41078325 seqs, 23393541228 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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CG103452 PUJBE19TB
CG082135 PUFQX12TD
CC630219 CQUCGS3TH
CC630210 CQUCGS3TH
CC6433618 PUFJAP6TD
AL175696 Tetraodon
BZ816318 PUFJAP6TD
CL997678 ZMMHHF07D
CCG201774 PUICH24TB
                                                                                                                                                                                                                                                                                                                                                                                                           CG252571 OG4BB05TC
CL235046 ZMMHBB057
CZ295176 ZMMBF0063
CG048704 PUILO19TB
CG414922 ZMMBBD029
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      404 ACCAGCCATGTCTAGTGTCCACTATTGGCACTACCCAGAACAAGATTTAAAAAAATAACC 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
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Mhitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Mhitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Compublished (2002)
Other GSSs: OGMOQ20TV
Contact: Cathy Whitelaw
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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/mol_type="genomic DNA"
/mol_type="genomic DNA"
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CG034985 PUICRSE8TB
BZ797976 PUBEPSETB
CC430754 PUHEPOSTB
CC435780 PUHSNO3TD
BZ78478 PUFHV09TD
BZ78478 PUFHV09TD
BZ78478 PUFHV09TD
BZ78478 PUFHV09TD
CC620594 OGUCC26TV
CC620594 OGUCC26TV
CC620594 OGUCC26TV
CC713918 OGJAG88TV
BZ676889 PUBIG1.TD
CC003943 PUJNK65TD
CC003943 PUJNK65TD
CC1994481 ZMMBH6000
CC1984151 ZMMBH6000
CC386762 PUHFK14TD
CC221693 OGMMG04TH
AL078714 DYOSODH1
DR794756 ZM BP5001
BZ996930 PUGIRSOTB
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq.primer: TF
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1 (bases 1 to 915)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OG1AG08TH
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                                                    CGATAGCCACCGTAATCATAGCTCATAGGTGCCTACGTCAGGTTCGGCAGCTCTCGTGTC 1160
                                                                                                     GGAGAGAGAGAGAAAATCAGTTTTAAGTCATTGTCCCTGAGATGTGCGGTTTGGCAA 1100
                                                                                                                                                         AAACCGAAACTGAAAATCGAGCGAAACCAAATCTGAGCTATTTCTCTAGATTAGTAAAAAG 1040
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/clone="Ibh="ZM_0.7_1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 679; DB 10;
Pred. No. 9.5e-132;
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539

479

419

359

980

299 920 860 179 800 119 740 59

これのこれ、一個大小人等等的機工事以上公司本

328

268

GSS 25-AUG-2003

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REFERENCE
AUTHORS
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CC656939/c
LOCUS
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                                    B
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Best Local Similarity
Matches 421; Conserv
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1129.GTGCCTACGTCAGGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTT
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                                                                                                                  567
                                                                                                                                                                                                                   949
                                                  507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 687)

Mitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGMD200TM
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCCTATTCTGAACCAAGAGGATACCTACTCCCAAACAATCCATCTTACTCATGCAACTT 1280
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                                                AGTCATTGTCCCTGAGATGTGCGGTTTGGCAACGATAGCCACCGTAATCATAGCTCATAG
                                                                                                                                                                                  TATAATTATTTGGCCAGCCCGATAAATTATTTAAACCGAAACTGAAATCGAGCGAAACCA 1008
                                                                                                                                                                                                                                                      GAAAAATAGAGTGCCCAGACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ass: methylation filtered.
Location/Qualifiers
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    /clone="ZMMBMa0554D15"
/clone lib="ZM 0.7 1.5_KB"
/bote="Vector: pBcSK: Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                      32.0%;
                                                                                                                                                                                                                                                                                                                     Score 419.8; DB 9; Pred. No. 2e-77; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rockville, MD 20850, USA
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                     1188
                                                                                     1128
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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AUTHORS
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CG252571/c
LOCUS
DEFINITION
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Best Local Sim
Matches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1189 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       447 GTGCCTACGTCAGGTTCGGCAGCTCTCGTGTCATCTCACATGGCATACTACATGCTTGTT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 CAACCGTTCGTCTTGTTCCATCGTCCAAGCCTTGCCTATTCTGAACCAAGAGGATACCTA
                                                                                                                                                             195 TCAGACACCTTTCGGGACACCCATCAAGGGCCTTTCGGATGGCCCCACGAGACGTATCGGG
                                                                                                                                                                                                                             135 TCTCCCACCTCGCGTTGCACATTTCTTGGATGTCGGTGGTTCCCATCTGACCGAGGCCCA 194
                                                                                                                                        296 TAAGGCACCTGTCGGAGAACCCATTAAAGGCCTTTTCGGATGGCCCACGGGACAT-CGGGG
                                                                                                                                                                                                          255 TCGTGGTGATCCAGGGGATATATGTCCCCCACAATC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 715)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG252571 715 bp DNA linear GSS 25-AU OG4BB05TC ZM_0.7_1.5 KB Zea mays genomic clone ZMMBMa0809B10, genomic survey sequence.
CG252571 CG252571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: methylation filtered.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                           h 7.3%;
Similarity 80.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC 265
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4577"
(clone="zwiBMa0809B10"
(clone="taxon:15_KB"
(clone="taxon: pBCSK-; Site 1: HincII; 0."
methylation filtered genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                          Score 96; DB 10; Length 71:
Pred. No. 1.5e-09;
0; Mismatches 30; Indels
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Length 715;

1;

Gaps

297

238 254 0.7-1

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SOURCE
ORGANISM
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AUTHORS
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KEYWORDS
                                 REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.0%;
Best Local Similarity 78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                               887
                                                                                                                                                                                                                                                                                                                                                                                                                             210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 967)
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronz Zohovetz,V., Fuke,G., Yu,Y., Wing,R. and Messing,J. Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CL235046 9

ZMMBBb0575001r ZMMBBb (Hin

ZMMBBb0575001 3', genomic

CL235046
                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                      CZ295176 860
ZMMBF0063M20f ZMMBF Zea mays
survey sequence.
CZ295176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 Frelinghuysen Road,
Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                               1 (bases 1 to 860)
Bharti, A.K., Nelson, A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bharti, A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
Construction, Sequencing
                 and Messing, J.
                                                                                                                   Zea mays
                                                                                                                                      Zea mays
                                                                                                                                                                        CZ295176.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: bharti@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                      GACACCCATCAAGGGCCTTTCGGATGGCCCACGAGACGTATCGGGTCGTGGTGATCCAGG
                                                                                                                                                                                                                                                                                                                                                 GGATATATGTCCCCCACAAT 289
                                                                                                                                                                                                                                                                                                                                                                                               GTGGCCCATCAAGTGCCTTTCGGATGGTCCACGGGATGTATCCGGGCCGTGTGACCTGGG
                                                                                                                                                                                                                                                                                                                             GGATATCTGTCCCCCATAGT 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGCCTTTCTTGGATACCGGCGGTTCCCGTCTGATTGAGGCCCCATCCAGCACCTTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence start: 64.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="ZMMBBb0575001"
/clone="ZMMBBb0575001"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Zea mays"
/mol_type="genomic D
/cultivar="B73"
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Pred. No. 1e-08;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piscataway,
 and
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                               Young, S.,
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genomic
 Characterization
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ic clone
                                 Keizer, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 967;
                                                                                                                                                                                                                          linear GSS
ZMMBF0063M20
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a
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                               Zohovetz, V.,
 Fosmid Library
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                                   Fuks, G
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RESULT 7
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Unpublished (2005)
Contact: Bharti, A
                                           9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                         Maize Genomics Consortium Unpublished (2003)
Other_GSSs: PUILO19TD Contact: Cathy Whitelaw
                                                                                                                                                                            1 (bases 1 to 814)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
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CG048704 CG048704.1 GI:33920884
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Seq primer: Fos_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute,
                                                                                                                                                                                                                                                                               Zea mays
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Class: sheared
              Seq primer: TR
                             Email: whitelaw@tigr.org
                                                                                                                                                                         Bennetzen, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GANATCCCTTGCTANTGATTGAGGGGGGAGAGAATTCGTAACTATCCA 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db xref="taxon:4577"
/clone="ZMMBF0063M20"
/lab host="EPI100-T1"
/clone_lib="ZMMBF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
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/note="Vector: pEpiFOS-5; Site_1:
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Pred. No. 1.7e-08;
0; Mismatches 85;
                                                                              Rockville,
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genomic
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i; Poales; Poaceae; PACCAD
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clone ZMM
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Length 754; Indels

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RESULT 8
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Matches 153;
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ZMMBBb0290L09.r ZMMBBb Zea mays
genomic survey sequence.
CG414922
CG414922.1 GI:34505144
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                                                                                                                                   Plate: 0290 row:
Seq primer: M13r
                                                                                                                                                                                        BACKWARD: M13r
                                                                                                                                                                                                                                                                                            Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of the maize genome 
Unpublished (2003)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                                                                                                                Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                             iological Sciences
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                                                                                                                                                                                                                                                                   rwing@genome.arizona.edu
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/clone="ZMMBTa6611C13"
/clone lib="ZM 0.6 1.0 KB"
/clone="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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/strain="B73"
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/organism="Zea mays"
/mol_type="genomic D
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                                                                                                                                                                  column:
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               241 ATCTTTCTAATGACTAGTTTGGGAACCTTATTT-TCTCACGGGATTTTTTATTTTTTCAAT 183
                                                                    787
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Zea mays
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1 (bases 1 to 950)
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Unpublished (2003)
Other GSSs: PUHRV15TD Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: TR
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  smail: whitelaw@tigr.org
                                                     ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAA 846
                                                                                                                         Conservative
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/note="Westor: pBeloBAC11; Site_1: HindII1; Site_2:
HindII1; Zea mays L. ssp. mays"
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                                                                                                                                                                                                                                                   /clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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                                                                                                                                                                                                                                                                                                                                           clone="ZMMBTa519D06"
                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:4577"
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71.2%; Pred. No. 7.8e-08;
Live 0; Mismatches 47
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                                                                                                                         Score 86.8; DB 9;
Pred. No. 1.3e-07;
0; Mismatches 47;
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Length 950; Indels

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Matches 131; Conserv
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maize Genomics Consortium Unpublished (2003) Other GSSs: PUHOC67TD Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Class: sheared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
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                                                                                                             TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAA
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nilarity 63.9%;
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/clone="zwMBTa495L13"
/clone_lib="ZM_0.6 1.0 KB"
/note="Vector: pCR4-TOFO; Site_1:
CoT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
/mol_type="genomic D
/strain="B73"
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Query Match
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CC400575 CC400575.1 GI:30880665
GSS.
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(bases 1 to 797)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Candon Miguel, P., Ma, J. and
                                                                                                                    CC400574 820 bp DNA linear GSS 19-N
PUHLUGITB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa480L01,
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Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
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ilarity 59.7%;
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4_TOPO; Site_1:
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/strain="B73"
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                                                                 GI:30880664
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Pred. No. 1.4e-07;
0; Mismatches 109;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773 CAAAAATCTTTCTGATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCCTTTCAAAGAATT 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 TTTAGAGGACGTTGGTAGAGATGGAAAGATATAGAGAAAAATAATCTTTTAGAGAAATGTTA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 TITATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTT 772
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                                                                                                                                                                                                                           PUURBLI9TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0628D13, genomic survey sequence.
CG103452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Other_GSSs: PUHLU61TD
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                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Epermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 471)
                                                                                                                                                   Zea mays
                                                                                                                                                                                        CG103452.1 GI:33985746
GSS.
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                                Whitelaw, C.A., Quackenbush, J., Va. Resnick, A., Fraser, C.M., Yuan, Y.,
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                                                                                                                                                                  sea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., lesnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                               AATTATTTGGCCAGCCCCATAAATTATTTAAAC 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATAGAGTTCTCAAACTAGCCCTAAGGTTATATCCGATAAATCCCCTATCTCATTCTCT
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                                                                                                                                                                                                                                                                                                                                                                            ATTTCAAATTCCACTTTGCAAAATAGTGTCATC 646
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telaw, C.A., Quackenbush, J.,
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Genomics Consortium
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 CoT selected genomic DNA library"
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/mol_type="genomic DNA"
/strain="B73"
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Pred. No. 1.4e-07;
0; Mismatches 109;
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                                Van Aken, S., Utterback, T., Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                   DNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUPOXIZID ZM 0.5.1.0 KB Zea mays genomic clone ZWMBTa0712B24, genomic survey sequence. CG082135.1 GI:33964429
CSG
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Other_GSSs: PUJBE19TD
                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopsid
clade; Panicoideae; Andropogoneae; Zea.
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Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                           Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUFQX12TB
                                                                                                                                                                                                                                                                                                                                                   Whitelaw, C.A., Quackenbur
Resnick, A., Fraser, C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays
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                                                                                                                      Class: sheared ends.
                                                                                                                                                                                                                                                         Contact: Cathy Whitelaw
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                                                                                                                                                                              Medical Center Drive,
301-838-5843
301-838-0208
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                                                                                                                                                         whitelaw@tigr.org
/mol_type="Zea mays"
/strain="B73"
/db_xref=".
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/mol_type="genomic DNA"
/strain="B73"
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/clone_lib="ZM_0.6_1.0_KB"
/note="Vector; pCR4-TOPO; Site_1: EcoRI; 0.6-1.0
CoT_selected_genomic_DNA_library"
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yta; Liliopsida; Poales; Poaceae; PACCAD
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San Miguel,P., Ma,J. and
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   847 AAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAAACACTTAGAAAAAATAGAGTTGCCAG 906
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Class: methylation filtered.
Location/Qualifiers
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CC630219
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WhiteLaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
WhiteLaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUCG53TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays
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                                                                                                                                                          ATTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTTGATTTTTTCAAA 846
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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/notes="Vector: pCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb
CoT selected genomic DNA library"
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                                                                                                             ACTAGCCCTAGAATGTTTTCCCAATAAATTACAATCACTGTGTATAATTATTTG 960
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Search Job tim

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Total number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/2/pubpna/US06]
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2100.307 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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(c) 1993 - 2006 Biocceleration
                  US-10-240-708-36
US-09-25-055A-803046
US-09-25-055A-803046
US-10-240-708-63
US-10-240-708-63
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US-11-991-883-182
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Sequence 2, Appli
Sequence 34, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 93046,
Sequence 73, Appl
Sequence 1314, Appl
Sequence 1314, Appl
Sequence 14, Appl
Sequence 26, Appl
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Sequence 667263,
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Sequence 182, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ ID NOS: 2
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 1092
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
FEATURE: (1)...(1092)
OTHER INFORMATION: P95
US-11-014-071-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Cigan, Andrew M.

APPLICANT: Cigan, Andrew M.

APPLICANT: Hox, Timothy W.

APPLICANT: Hershey, Howard P.

APPLICANT: Wu, Yongzhong

APPLICANT: Wu, Yongzhong

ITITLE OF INVENTION: Methods of Using Same

ITITLE OF INVENTION: Methods of Using Same

ITITLE OF INVENTION: Methods of Using Same

ITILE OF INVENTION: MOMBER: US/11/014,071

CURRENT APPLICATION NUMBER: US/11/014,071

CURRENT APPLICATION NUMBER: US/13/478

PRIOR APPLICATION NUMBER: 00/530,478

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Best Local Similarity 57.3%;
Matches 142; Conservative
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                                                                                                                    391 ACATAGTTTAGATTCAGTCAGCAAAAAGCTAACATTATGTTTGCTTCTTTTATTCATATA
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No. US20050246796A1
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8 US-10-240-708-10

8 US-10-240-708-3

8 US-10-240-708-46

8 US-10-240-708-42

8 US-10-240-708-9

10S-10-240-708-9

10S-11-21-312A-90

6 US-9-925-065A-714060

12 US-11-011-332A-91

12 US-11-011-332A-91
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6 US-09-925-065A-206150
8 US-10-240-708-74
12 US-11-011-32A-96
12 US-10-330-773-242
12 US-11-011-32A-76
13 US-10-330-773-815
18 US-10-340-708-13
19 US-10-340-708-13
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0.0063;
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sequence 74, Appl
Sequence 74, Appl
Sequence 96, Appl
Sequence 242, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 25, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 35, Appl
Sequence 90, Appl
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Minimum DB seq length: 0
Maximum DB seq length: 200000000

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Query Match Length

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Scoring table:

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CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
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US-10-240-708-36
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 36, Application US/10240708
Publication No. US20050282157A1
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LENGTH: 9347
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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 TAAGATTTTATTTTGTT
                                 AAAATTAGTTTATTTT 863
                                                                         ATTTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTCAAAGAATTTTGATTTTTTCAAA 846
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8846
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Pred. No. 0.64;
0; Mismatches 162; Indels
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; ORGANISM: Homo sapiens
US-10-330-773-534
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Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEC ID NOS: 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version SEQ ID NO 534
LENGTH: 254396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                            201431
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TTTGTCATAATTGTAATCATTTTAGGCTTTTTTAAAAA 201648
                                                                    AGAATCAAATGGCATTAGAATTTAGAACAACTTCTAAATCATCGTGAGGTATTTTTCCTAT 201610
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                                                                                               CGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGATTTTTTTAAGAGCTAGTTTGGCAA 811 ·
                                                                                                                                        ATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAGTCATTTTTATATAAGAGCA
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0; Mismatches 214;
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Pred. No. 3
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT PILLING DATE: 2001-08-08
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092

APPLICATION NUMBER:

60/289,846

US-09-925-065A-54272

Sequence 54272, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-54272
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US-09-925-065A-803046
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SEQ ID NO 803046
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Best Local
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NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRANCESQ for Windows Version 4.0
SEQ ID NO 54272
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Best Local
                                                                                                                       Matches 137;
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CURRENT FILING DATE: 2001-08-08
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 108827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Wang, David G.
ITLE OF INVENTION: Identification and Mapping of Single
ITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656 TIGITATIGITITATATACATITITCT-TCTCTTACAATAGAGIGAGITGATTTTCTTCCGATTT 714
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FastSEQ for Windows Version 4.0
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Similarity 51.0%;
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Pred. No. 1.2;
1; Mismatches 143;
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US-10-240-708-73/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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CURRENT APPLICATION NUMBER: US/10/240,708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT: BERLIN, Kurt
TTLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TTLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 5152
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FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                    4077
                                                        4137 СТАСААТСССААСТАСТСАААААТСТСАААСААААААТААСТТАААСССАААААТТСАА
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277 TGTTCTTTTTTTTTTTTTTTAGAAAAAAAAAACACTT
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                                                                                                                                                                                                                                                                    AACTATCATAAACCGTAATTACGCCACTACATTTCAACCTAAACAAAAAACAAAACCCTA 4018
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No. US20050282157A1
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 3;
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APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION. Diagnosis of Disease Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 63
             RESULT 8
US-10-995-561-13314/c
Sequence 13314, Application US/10995561
Publication No. US20050272054A1
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US-10-240-708-63
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US-10-240-708-63
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GENERAL
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 140; Conserv
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INFORMATION
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                                                                                                                                                                                                                                 TTTTTTTTTTTTTTTTTAAGAAA 1591
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ilarity 52.4%;
Conservative
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Pred. No. 3.3;
0; Mismatches
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PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                      Sequence 803045, Application US/09925065A Publication No. US20040181048A1 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13314
LENGTH: 119036
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Best Local Similarity
                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827, 135
CURRENT FILLING DATE: 2001-08-08
CURRENT FILLING DATE: 2001-08-08
FRIOR APPLICATION NUMBER: US 60/243,096
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: n =
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Pred. No. 7
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                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-708-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-803045
                                                                           Query Match
Best Local Simi
Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 803045
LENGTH: 488
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Best Local
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SEQ ID NO 11
LENGTH: 6317
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION UNMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
                                                                                                                                                             TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: OLEK, Alexander PPLICANT: PIEPENBROCK, Christian
                 217
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al Similarity 48.9%;
136; Conservative
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                                                                                       3.98;
                                                                         ; Score 51.6; DB; Pred. No. 7.1; 0; Mismatches
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Pred. No. 3.3;
1; Mismatches 141; Indels
                                                                                                         DB 8;
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Best Local Similarity
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ORGANISM: Homo sapiens
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RESULT 11
US-10-330-773-242/c
US-10-330-773-242/c
Sequence 242, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION
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LENGTH: 355211
TYPE. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1)...(355211)
OTHER INFORMATION: n = A,T,C'or G
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                                                                                                                                                                                                                                                                                                                      503 AAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTTCGAAAGAGACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                  443 ACAAGATTTAAAAAAATAACCAAAGTAACTAATCCACTCGAAAGCTATCATGTAATGTTT
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TCTCTTACAATAGAGTGATTTTCTTCCGATTTTATAAAATGACTATAAAAGTCATTTTAT 742
                                                  AATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAAGGTAAGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ilarity 46.1%;
Conservative
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Pred. No. 1
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APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

APPLICANT: NIELSEN, KIRSTEN V.

TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACI

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR PILLING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PatentIn version 3.3
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LENGTH: 173602
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Local Similarity 45.5%;
38 219; Conservarium
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                        CGACAAATTATATCGAAAGGTAAGCTATGACGTTCAGATTTTTCTTTTTCATTCTTTA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĀTATĀTTĀTĀTĀTTĀTĀTGTTTĀTGTĀTĀTĀTĀĀĀTĀTĀTĀĀT-ĀTĀTĀĀĀTĀTTTTA 136597
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                                                                                                                                                                    TGATTTTTTCAAAAAAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAA 893
                                                                                                                                                                                                         TTATAAAATGACTATAAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTC 773
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Pred. No. 17;
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RESULT 14

US-09-925-065A-667262
; Sequence 667262, Application US/09925065A
; Sequence 667262, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human G
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
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US-10-330-773-26
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Best Local :
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APPLICANT: Marc Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1)...(68741
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                                                                                                                                                                                                                                                                TATAAATA 465
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llarity 46.2%;
Conservative
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Pred. No. 25;
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                                                                              in the Human Genome
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RESULT 15
US-09-925-065A-667263
Sequence 667263, Application US/09925065A
Sequence 667263, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION: US20040181048A1
GENERAL INFORMATION: Identification and Mapping of Single
TITLE OF INVERTION: Nucleotide Polymorphisms in the Human Gence
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION DATE: 2001-01-16
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEG for Windows Version 4.0
SEQ ID NO 667262
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; ORGANISM: Homo sapiens
US-09-925-065A-667262
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Best Local :
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    Mismatches

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Best Local S
Matches 214
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PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOPTWARE: FASTSEQ.for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO 667263
ENGTH: 677
                                                                                                                                                                                                                                                                                                                                                                                          492 AUGTAATGTTTAAAGAAACATCTATTAAAACCACGATCCTCTTAAAAAACAAGCATATTT
                                                                                                                                                                                                                                                                                                                                       552 CGAAAGAGACAAATTATGTTACAGTTTACAAACATCTAAGAGCGACAAATTATATCGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                     214;
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                                                                                                                                                                                                                                                           789 TTTTTTAAGAGCTAGTTTGGCAACCCTGTTTCTTTCAAAGAATTTTGATTTTTTCAAAAA 848
                                                                                                                                                                             729 AAAGTCATTTTTATATAAGAGCACGCATGTCGTAGATTCTCGTTCAAAAATCTTTCTGAT 788
                                                                                                                                                                                                                              672 ATACATTTTCTTCTTTACAATAGAGTGATTTTCTTCCGATTTTATAAA----ATGACTAT 728
909 TAGCCCTAGAATGTTTTCCCCAATAAATTACAATCACTGTGTATAATTAT
                                                  849 AAATTAGTTTATTTTCTCTTTATAAAATAGAAAACACTTAGAAAAATAGAGTTGCCAGAC 908
                                                                                                                                                                                                         Similarity
                                                                                                                                                        Conservative
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